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SEARCH REQUEST FORM

Scientific and Technical Information Center

CRFE

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Requester's Full Name: 1. A. M Art Unit: 1652 Phone Nu Mail Box and B)dg/Room Location:	mber 305 - 727 C	Carial Number: 10	Date: March 11, 03 050, 200 PAPER DISK E-MAIL
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Include the elected species or structures, ke utility of the invention. Define any terms the	hat may have a special me	raning. Give examples or releva	ant citations, authors, etc, if
Title of Invention: Dy garte Co. Inventors (please provide full names):	FOURIE A	et of	les ond menuous
Inventors (please provide full names):	1 00 101 22 11		•
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	HIV-1 vaccine synt	chimer	chimer:	pept	ptic	ч	Chimaeric T/B cell	V3 cons	56/P24M	P24M/CLTB-56 chime	7	chimeric	eptide ep	Chimaeric T/B cell	a	GAG segment	-1 p24 epito	protein T-	DR 3a motif	DR 3a moti	1 vaccine	1 gag prote	peptide	T-helper c	ell epitope, P	1, gag 357-370	B27 super	B27 super	protease cle	27 super	an immunodefi	tease pepti	B58 super mot	A02 super mo	HIV A03 motif gag

ALIGNMENTS

ABB80017; 17-JUL-2002

(first entry)

ABB80017 standard; peptide; 10 AA.

DE Cathepsin S inhibition assay substrate peptide.

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XX

Cathepsin S; antiallergic; antiasthmatic; dermatological; pyra:

KW atopic allergy; hay fever; asthma; atopic dermatitis; food alla

KW allergy; dust; pollen; mold; pet dander; pet hair.

XX

Unidentified.

XX

FH

Key

FT

Modified-site

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Note= "C-terminal amide"

XX

VX

VX

V200220011-A2.

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V3-SEP-2001; 2001WO-US27429.

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Butler CR, Karlsson L,

Cai H, Edwards JP, Grice CA, (Khatuya H, Meduna SP, Pio BA,

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n DJ; Sun S; (ORTH) ORTHO-MCNEIL PHARM INC

06-SEP-2000; 10-AUG-2001;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Treatment
                                                                                                                                                                                                                                                                                                                         Human cathepsin
                                                                                                                                                                                                                                                                                                                                                                                AAU80096 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       comprises
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                                                                                                                                                                                                                                                                                            Cathepsin S; allergy; pyrazole; hay fever; asthma; atopic food allergy.
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10-AUG-2001;
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                allergic conditions, allergies, comprises
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administration
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tive 0;
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                                                                                            PHARM INC.
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                                                                                                                                                                                                                   "Dabcyl"
                                                                                                                                                                                                                                      "Aedens-Glu"
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                                                                                                                                                                                                                                                                                                                                                                                 11
                                                                                                                                                                                                                                                                                                                         peptide
                                                                         Karlsson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 44;
Pred. No.
               e.g. hay fever, asthma, atopic dermatiti administration of a substituted pyrazole
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RESULT 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         pyrazole (I) or a salt, amide or ester. The method is used for treating allergic conditions, e.g. hay fever, asthma, atopic dermatitis and food allergies. The present sequence represents human cathepsin S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to a method of treating allergic comprising administration of a composition comprising a
                               The present sequence is a peptide used as substrate for a cathepsin S inhibition assay. The Kmm for the substrate is arou by but the presence of substrate inhibition makes kinetic analysis difficult. With 20 uM substrate, the assay rate is linear over the range of 1-8 ng cathepsin S in 100 ul reaction. Using 2 ng/well of cathepsin S, the production of product is linear and yields about 7-fold signal after 20 min with only 20 loss of substrate. Primary assays are run by quenching the
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reaction after 20 min and then measuring the other assays, measurements are taken every mi rate is calculated from the slope of the incr
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                                                                                                                                         Page 29;
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fasthmatic; dermatological;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pred. No. is the number of results predicted by chance to have score greater than or equal to the score of the result being pand is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                Score
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86.4
86.4
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Match
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| SIDS1/gcgdata/geneseq/geneseqp-embl/AA1980.DAT:*
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Listing first 45 summaries
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SIDSI/gcgdata/geneseq/geneseqp-embl/AA1990_DAT:

SIDSI/gcgdata/geneseq/geneseqp-embl/AA1990_DAT:

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	syn	chimeric	ric pep	tide epi	peptide epi	T/B cel	ri	P24M/V3 consensus	56/P24M	M/CLTB-56 c	1 vaccine syn	per	peptide epi	Chimaeric T/B cell	P24M/V3 consensus	GAG se	-1 p24 epitop	protei	DR 3a motif g	DR 3a motif g	1 vaccine syn	'n	-1 peptide epi	T-helper dete	ll epitope, P	1, qag 357-370	B27 super mot	B27 super	protease clea	super mot	an immunodefi	tease peptide.	B58 super mo	A02 super mot	نم

ALIGNMENTS

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ABB80017
ID ABB8
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                                                                                                                                                                                                                                                                                                                                                                             05-SEP-2001; 2001WO-US27429.
    Butler CR,
Karlsson L,
                                                                                                                                                                                                                                            06-SEP-2000; 2000US-230407P.
10-AUG-2001; 2001US-0927324.
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                                                                                                                                               (ORTH ) ORTHO-MCNEIL PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Modified-site
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Cai H, Edwards JP, Grice CA, G
, Khatuya H, Meduna SP, Pio BA,
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Best Local
                                            Treating allergic conditions, and food allergies, comprises
                                                                                                                  WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to the treatment of allergic conditions, comprising the administration of a pyrazole derivative. The activity of derivatives of the invention may be described as, antiallergic, antiasthmatic and dermatological. They act as cathepsin S inhibitors and may be used for the treatment of allergic conditions including atopic allergies, e.g. hay fever, asthma, atopic dermatitis, food allergies and allergies to dust, pollen, mold, pet dander or pet hair. The current sequence represents a cathepsin S inhibition assay substrate peptide.
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10-AUG-2001;
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                                                                                                                                                            Thurmond
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1 RL, Wei J;
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2001US-0927188.
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Pred. No.
                                         e.g. hay fever, asthma, atopic administration of a substituted
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                                                                                                                               The present sequence is a peptide used as substrate for a cathepsin S inhibition assay. The Km for the substrate is aroung the bull of the presence of substrate inhibition makes kinetic analysis difficult. With 20 uM substrate, the assay rate is linear over the range of 1-8 ng cathepsin S in 100 ul reaction. Using 2 ng/well of cathepsin S, the production of product is linear and yields about 7-fold signal after 20 min with only 20% to the product of th
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cathepsin S; inhibitor; allergy; hay fever; asthma; food allergy; atopic dermatitis; antiallergic; antiasthmatic; dermatological; antiinflammatory; immunosuppressive.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to a method of treating allergic conditions comprising administration of a composition comprising a substituted pyrazole (I) or a salt, amide or estar altergic conditions, e.g. hay fever, asthma, atopic dermatitis and food allergies. The present sequence represents human cathepsin S substrate peptide used in an assay to demonstrate the method of the
loss of substrate. Primary assays are run by quenching the reaction after 20 min and then measuring the fluorescence. other assays, measurements are taken every min for 20 min. rate is calculated from the slope of the increase and the pe
                                                                                                                                                                                                                                                                                                                                                                                                                      Example
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Modified-site
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ) ORTHO-MCNEIL PHARM INC
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RESULT 4
AAU83139
The invention describes an isolated mammalian secreted polypeptide (MSP) (C (I) (I) is useful to direct the secretion of other proteins of interest from a host cell, to monitor secretion of proteins, to degenerate sequences comprising all nucleotide sequences encoding a particular polypeptide, to screen for cell metabolism effecting receptors, for identifying new target receptors and drug design, for identifying, for complimental protein purification, for determining the weight of expressed MSP completed as a ratio to total protein expressed, for identifying peptide cleavage sites, for coupling amino and carboxy terminal tags, for manno acid sequence analysis, for monitoring biological activities of the protein in vitro and in vivo, and to teach analytical skills and as reagents for the study of cells, receptors, and other binding molecules. The polynucleotide is useful for radiation hybrid mapping, and somatic contiguous maps of mammalian chromosomes. Reagents disclosed in the invention may be used to detect metabolic abnormalities characterised by over or under production of the protein. This is the amino acid sequence of a mammalian secreted polypeptide, described in the method of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel isolated mammalian secreted polypeptide useful in therapeutic and diagnostic methods, to direct secretion of other proteins of interest from host cell, as educational tools, and as laboratory practicum kits
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Pred. No. 0.034;
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RESULT 5
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Best Local S
Matches
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Best Local
                       Matches
                                                                                                                                                                                                                                                                     Ota T, Ishii S, S
                                                                                                                                                                                                                                                                                                                                                                                     29-JUL-1999;
27-AUG-1999;
18-OCT-1999;
                                                                                                                             The present sequence is encoded by a liver-associated gene. The expression level of this gene changes in liver (hepatic) cancer expression level of this gene changes in liver (hepatic) cancer liver-associated gene can be used as markers in blood tests for the liver-associated gene can be used as markers in blood tests for the liver-associated gene.
                                                                                                                                                                                              New genes and their proteins found in hepatic cancer, vectors, antibodies, and screening method for compounds with binding acuseful as diagnostics and targets for treatment agents -
                                                                 Sequence
                                                                                   screening for the early stages of the liver cancer proteins and peptides can also be used as targets for compounds to treat the disease. They can also predicting the progress of the disease.
                                                                                                                                                                           Claim 1;
                                                                                                                                                                                                                                                                                                                                            09-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                      02-MAY-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HOMO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Liver-associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Amino acid sequence of a human liver-associated gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAG67257;
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                                                                                                                                                                                                                                                                                                                                                                 17-FEB-2000;
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  1 EKARVLAEAA 10
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2 EKSRLLAEAA 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sapiens
                                                                                                                                                                                                                                          2001-541221/60.
DB; AAH77810.
                      Similarity
8; Conserv
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8; Conser
                                                                                                                                                                                                                                                                                                                      HELIX RES INST.
                                                                                                                                                                                                                                                                                                 Isogai T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             standard; Protein; 396
                                                                                                                                                                          Page 79-80;
                                                                                                                                                                                                                                                                          Sugiyama T
Hippo Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          219
                                                                 396 AA;
                                                                                                                                                                                                                                                                                                                                           2000JP-0118776.
2000US-0183322.
2000JP-0183767.
2000JP-0241899.
                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                 2000WO-JP05064.
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A
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99US-0159590.
                                                                                                                                                                                                                                                                                                                                                                                                            99JP-0248036
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gene; hepatic cancer; liver cancer; marker.
                                                                                                                                                                                                                                                                         Nishikawa T, F
b T, Wakamatsu A
Y, Taniguchi H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      86.4%;
80.0%;
                                 86.4%;
                                                                                                                                                                          99pp; Japanese.
                                                                                                    be used as markers in blood recorded tages of the liver cancer. The encoded tages of the largets for screening
                     Score 38; DB Pred. No. 19; 2; Mismatches
                       <u>ب</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
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Pred.
                                                                                                                                                                                                                                                                                    Hayashi K, S
A, Nagai K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      No.
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11;
                               DB
19;
                                           22;
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                                                                                                                                                                                                                                                                                      Saito K,
Otsuki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
                                           Length 396;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 219;
                                                                                                 be used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                     Yamamoto J; T, Aburatan
                                                                                                 for
                                                                                                                                                                                                                                                                                      Aburatani
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                                                                                                                                                                                                           activity,
                     Gaps
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RESULT 6
AAB94593
ID
AAB94593
XX
AAB94593
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AAB94593
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Huma
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Huma
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Huma
XX
Huma
XX
Huma
XX
PF 28-J
PF 28-J
PR 11-J
PR 11
В
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                                                                                                                                                                                                                                                                                   of an oligonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 5'-end sequence and an oligonucleotide comprising a sequence complementary to a polynucleotide which comprises a sequence complementary to a polynucleotide which comprises at least 15 nucleotides and the combination of the 5'-end sequence/3'-end sequence is selected from those defined in the specification. The primers sets can be used in antisense therapy and in gene therapy. The primers are useful for synthesising polynucleotides, particularly full-length cDNAs. The primers are also useful for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers allow obtaining of the full-length cDNAs. The primers allow obtaining of the full-length and AAH13633 to AAH18742 represent human cold sequences; AAB92446 to AAB95893 represent human amino acid sequences; AAB9245 to AAH13632 represent oligonucleotides, all of which are used in the exemplification of the present invention.
                                                                                                                     Matches
                                                                                                                                              Query Match
Best Local
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27-AUG-1999;
11-JAN-2000;
02-MAY-2000;
09-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention describes primer sets for synthesising 5602 full-length cDNAs defined in the specification. Where a primer set comprises: (a) an oligo-ord primer and an oligonucleotide complementary to the complementary strand of a polynucleotide which comprises one of the 5602 nucleotide sequences defined in the specification, where the oligonucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprising a sequence complementary to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs
                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2001-318749/34.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; primer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26-JUN-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (HELI-) HELIX RES INST.
229
                                                   EKARVLAEAA 10
EKSRLLAEAA 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8; SEQ ID 15405; 2537pp + CD ROM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  protein
                                                                                                               8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Isogai T, Sugiyama
                                                                                                                                                                                                                                     396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            99JP-0248036.
99JP-0300253.
2000JP-0118776.
2000JP-0183767.
2000JP-0241899.
                                                                                                               Conservative
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                                                                                                                                                                                                                                     AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nishikawa T,
T, Wakamatsu
                                                                                                                                              80.0%;
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                                                                                                                                              Score 38; Pred. No.
                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hayashi K,
A, Nagai K,
                                                                                                                                        . 19;
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                                                                                                                                                                            22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Saito K,
Otsuki
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                                                                                                                                                                         Length 396;
                                                                                                                  Indels
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RESULT 7
AAY74531
IDY AAY7
XX AAY7
XX Neis
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                                                                                                                    Query Match
Best Local
                                                                                                Matches
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31-JUL-1998;
02-SEP-1998;
02-SEP-1998;
09-OCT-1998;
09-OCT-1998;
09-OCT-1998;
25-FEB-1999;
                                                                                                                                                                                                                                    AAZ53015 to AAZ54536, AAZ54577 to AAZ54615, and AAY74253 to AAY75941 represent novel Neisseria meningitis and N. gonorrheae polynucleotides and polypeptides. AAZ54537 to AAZ54576 and AAZ54616 to AAZ54473 represent PCR primers used in the exemplification of the present invention. The polypeptides, the polynucleotides, antibodies and compositions of the invention can be used as vaccines, as diagnostic reagents, and as immunogenic compositions. The polypeptides can be used in the manufacture of medicaments for treating or preventing infection due to Neisserial bacteria (e.g. meningitis and septicaemia), to detect the presence of Neisseria bacteria, or to raise antibodies. They may also be used to screen for agonists or antagonists, which may themselves have use as antibacterial agents. The polynucleotides of the invention may also be used in gene therapy protocols.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Neisseria meningitidis; Neisseria gonorrheae; antigenic; diagnosis; immunogenic; infection; antibacterial; gene therapy.
                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel Neisserial polypeptides predicted vaccines and diagnostics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Petersen J,
Tettelin H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Fraser C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (CHIR )
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11
                                        1 EKARVLAEA 9
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DB; AAZ53293.
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                                                                                                                    Similarity
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INST GENOMIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Galeotti C, Grandi G,
, Pizza M, Rappuoli R,
                                                                                                                                                                                              298
                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pizza M,
Venter JC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
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98US-0094869.
98US-0099062.
98US-0103749.
98US-0103794.
98US-0103794.
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                                                                                                                    Score 36;
Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        protein sequence
                                                                                                Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hickey
Ratti
                                                                                                                  . 36;
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                                                                                                                                           21;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 meningitis; septicaemia;
                                                                                           0
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Scalato E, Scarselli
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                                                                                                                                           Length 298
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RESULT 8
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RESULT 9
AAY74533
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Best Local :
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Petersen J,
Tettelin H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         09-OCT-1998;
09-OCT-1998;
09-OCT-1998;
25-FEB-1999;
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02-SEP-1998;
02-SEP-1998;
                                                                                                                                                                                                                                                                                                                                                            AAZ53015 to AAZ54536, AAZ54577 to AAZ54615, and AAY74253 to AAY75941 represent novel Neisseria meningitis and N. gonorrheae polynucleotides and polypeptides. AAZ54537 to AAZ54576 and AAZ54616 to AAZ5473 represent PCR primers used in the exemplification of the present invention. The polypeptides, the polynucleotides, antibodies and compositions of the invention can be used as vaccines, as diagnostic reagents, and as immunogenic compositions. The polypeptides can be used in the manufacture of medicaments for treating or preventing infection due to Neisserial bacteria (e.g. meningitis and septicaemia), to detect the presence of Neisseria bacteria, or to raise antibodies. They may also be used to screen for agonists or antagonists, which may themselves have use as antibacterial agents. The polypucleotides of the invention may also be used in gene therapy protocols.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Neisseria meningitidis; Neisseria gonorrheae; antigenic; diagnosis; immunogenic; infection; antibacterial; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (CHIR )
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 2; Page 390-391; 1453pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel Neisserial polypeptides predicted to vaccines and diagnostics -
                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-MAY-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11-NOV-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Neisseria meningitidis
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                                                                                                        11 DKARILAEA 19
                                                                                                                                1 EKARVLAEA 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2000-062150/05.
DB; AAZ53294.
                                                                                                                                                                                                        Similarity 7; Conserv
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INST GENOMIC
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, Pizza M, Rappuoli R,
, Venter JC;
                                                                                                                                                                                                                                                                                                                   298 AA;
                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      98US-0093758.
98US-0094869.
98US-0098994.
98US-0099062.
98US-0103749.
98US-0103794.
98US-0103794.
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                                                                                                                                                                                                                                      81.8%;
77.8%;
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                                                                                                                                                                                                        Score 36; DB Pred. No. 36; 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         English.
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Ratti G,
                                                                                                                                                                                                                                                            21;
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meningitis; septicaemia;
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Scalato E, Scarselli M;
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                                                                                                                                                                                                                                                               Length 298;
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RESULT 10 ABP12631 ID ABP12 XX

ABP12631 standard; Peptide;

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11

DKARILAEA

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                             Matches
                                        Query Match
Best Local
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Petersen J,
Tettelin H,
                                                                                                    represent novel Neisseria meningitis and N. gonorrheae polynucleotides and polypeptides. AAZ54537 to AAZ54576 and AAZ54616 to AAZ5447 represent PCR primers used in the exemplification of the present invention. The polypeptides, the polynucleotides, antibodies and compositions of the invention can be used as vaccines, as diagnostic reagents, and as immunogenic compositions. The polypeptides can be used in the manufacture of medicaments for treating or preventing infection due to Neisserial bacteria (e.g. meningitis and septicaemia), to detect the presence of Neisseria bacteria, or to raise antibodies. They may also be used to screen for agonists or antagonists, which may themselves have use as antibacterial agents. The polypucleotides of the invention may also be used in gene therapy protocols.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Neisseria meningitidis; Neisseria gonorrheae; antigen; vaccine; antigenic; diagnosis; immunogenic; infection; meningitis; septicaemia; antibacterial; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-MAY-1998;
31-JUL-1998;
                                                                                                                                                                                                                                                                                                                                                                  N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           (CHIR )
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Neisseria meningitidis.
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                                                                               Sequence
                                                                                                                                                                                                                                                                     AAZ53015 to AAZ54536, AAZ54577 to AAZ54615, and AAY74253 to AAY75941
                                                                                                                                                                                                                                                                                              Claim 2; Page 392; 1453pp; English.
                                                                                                                                                                                                                                                                                                                         Novel Neisserial polypeptides predicted to vaccines and diagnostics -
                                                                                                                                                                                                                                                                                                                                                                  WPI; 2000-062150/05.
N-PSDB; AAZ53295.
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09-OCT-1998;
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09-OCT-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Neisseria meningitidis ORF 138 protein sequence SEQ ID NO:540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    25-FEB-1999;
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  1 EKARVLAEA 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                          CHIRON CORP.
INST GENOMIC RES.
                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                     Galeotti C, Grandi G,
, Pizza M, Rappuoli R,
, Venter JC;
                                                                                 298
                             Conservative
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98US-0099062.
98US-0103749.
98US-0103794.
98US-0103796.
99US-0121528.
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98US-0094869.
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                                        81.8%;
77.8%;
                           2
                                       Score 36; DB Pred. No. 36;
                             Mismatches
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Ratti
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                                                     21;
                                                                                                                                                                                                                                                                                                                                       be useful antigens
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Scalato E, Scarselli
                                                   Length 298;
                             Indels
                           0
                          Gaps
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RESULT 11
ABP20832
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                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sette A,
Baker DM,
 15-JUL-2002
                               ABP20832;
                                                             ABP20832 standard;
                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2001-354887/37.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     05-OCT-2000; 2000WO-US27766
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO200124810-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human immunodeficiency virus type 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HIV; HIV-1; human immunodeficiency virus; env; pol; gag; nef; vpr; vpu; vif; tat; cytotoxic T lymphocyte; CTL; immune response; epitope; antigen; vaccine; HIV infection; immunisation; virucide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1) peptide groups, useful for vaccinating against HIV-1 -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       05-0CT-1999;
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                                                                                                                                                                           2 KARVLAEA 9
                                                                                                                                             KARVLAEA 8
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Celis E,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Page 127; 448pp; English.
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                                                                                                                                                                                                           Conservative
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(first entry)
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                                                             Peptide;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Southwood Kubo RT,
                                                                                                                                                                                                         0;
                                                                                                                                                                                                                      Score 35; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     d S, Livi
                                                                                                                                                                                                           Mismatches
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                                                                                                                                                                                                                        DB 22;
7.8e+05;
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                                                                                                                                                                                                                                     Length 8;
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RESULT 12
ABP12751
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                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sette A,
Baker DM,
                                                                                                              ABP12751 standard; Peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HIV; HIV-1; human immunodeficiency virus; env; pol; gag; nef; vpr; vpu; vif; tat; cytotoxic T lymphocyte; CTL; immune response; epitope; antigen; vaccine; HIV infection; immunisation; virucide.
                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 32; Page 296; 448pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1) peptide groups, useful for vaccinating against HIV-1 .
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                                                                                                                                                                                                                             2 KARVLAEA 9
                                                                                                                                                                                                KARVLAEA
                                                                                                                                                                                                                                                              Similarity
8; Conserv
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Celis E,
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                                                                                                                                                                                                                                                              Conservative
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                                                                                                                                                                                                                                                                                79.5%; Score 35; 100.0%; Pred. No.
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                                                                                                                                                                                                                                                                0:
                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                DB 22; 1
7.8e+05;
hes 0;
                                                                                                                                                                                                                                                                                              Length 8;
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HIV A02 super motif gag peptide #222

15-JUL-2002 (first entry)

ABP12751;

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RESULY 13
ABP17961
ID ABP17
XX ABP17
AC ABP17
XX 15-JU
DT 15-JU
DE HIV B
XX HIV;
KW YPU;
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                                                                                                                                                                                                                                                                                                                                                                                                                                           CC The present invention describes a composition (1) comprising a prepared CC human immunodeficiency virus-1 (HIV-1) group comprising an amino acid Sequences selected from 51 defined amino acid sequences (ABL25347 to CC ABP25397). (1) has virucide activity and can be used in vaccines. (1) CC may be used for immunising subjects against HIV-1 infections. The use of group-based vaccines has several advantages over traditional vaccines (2 particularly when compared to the use of whole antigens in vaccine CC compositions. There is evidence that the immune response to whole CC antigens is directed largely toward variable regions of the antigen, and group-based vaccine may be selected from conserved regions of viral or tumour-associated antigens, which therefore reduces the likelihood of CC escape mutants. Furthermore, immunosuppressive groups that may be present in whole antigens can be avoided with the use of group-based vaccines. An additional advantage of an group-based vaccine approach is the ability to combine selected groups (CTL and HTL), and further, to modify the CC immunogenicity. Accordingly, the immune response can be modulated, as cappropriate, for the target disease. Similar engineering of the response cinvention.

CC invention.
                                                                                                                                                                                                                                                                                                                                  Matches
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HIV; HIV-1; human immunodeficiency virus; env; pol; gag; nef; vpu; vif; tat; cytotoxic T lymphocyte; CTL; immune response; e antigen; vaccine; HIV infection; immunisation; virucide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HIV: HIV-1; human immunodeficiency virus; env; pol; gag; nef; vpr; vpu; vif; tat; cytotoxic T lymphocyte; CTL; immune response; epitope; antigen; vaccine; HIV infection; immunisation; virucide.
                                                                                                                                          ABP17961
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1) peptide groups, useful for vaccinating against HIV-1 -
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                                                                 HIV B58 super motif gag peptide #180.
                                                                                                         15-JUL-2002
                                                                                                                                                                       ABP17961 standard; Peptide;
                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                      Invention
                                                                                                                                                                                                                                                                                                                                              Local
                                                                                                                                                                                                                                                                1 KARVLAEA 8
                                                                                                                                                                                                                                                                                             2 KARVLAEA 9
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                                                                                                                                                                                                                                                                                                                                Similarity
8; Conserv
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Celis E,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Page 130; 448pp; English
                                                                                                                                                                                                                                                                                                                                                                                                    9
                                                                                                                                                                                                                                                                                                                                Conservative
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                                                                                                       (first entry)
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                                                                                                                                                                                                                                                                                                                                                79.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Southwood S, Livingston BD, Kubo RT, Grey HM;
                                                                                                                                                                         v
                                                                                                                                                                                                                                                                                                                                0:
                                                                                                                                                                                                                                                                                                                                              Score 35; DB 22;
Pred. No. 7.8e+05;
                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                0
                                                                                                                                                                                                                                                                                                                                                               Length 9;
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RESULT 14
AAE19118
ID AAE19
XX AAE19
AC AAE19
AC AAE19
XX Z1-M2
XX Z1-M2
XX Lucif
XW Cell
XX Cell
XX Unide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cc human immunodeficiency virus-1 (HIV-1) group comprising an amino acid composition of the virus-deficiency virus-1 (HIV-1) group comprising an amino acid compositions acted from 51 defined amino acid sequences (ABL25347 to CC ABP25397). (1) has virucide activity and can be used in vaccines. (1) compositions when compared to the use of group-based vaccines has several advantages over traditional vaccines. CC particularly when compared to the use of whole antigens in vaccine compositions. There is evidence that the immune response to whole callowing for immune escape due to mutations. The groups for inclusion in callowing for immune escape due to mutations. The groups for inclusion in composition for immune escape due to mutations. The groups for inclusion in composition antigens, which therefore reduces the likelihood of composition antigens can be avoided with the use of group-based vaccines. An additional advantage of an group-based vaccine approach is the ability to combine selected groups (CTL and HTL), and further, to modify the composition of the groups, achieving, for example, enhanced in the composition of the groups, achieving, for example, enhanced as a compropriate, for the target disease. Similar engineering of the response continuous for the target disease. Similar engineering of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1) peptide groups, useful for vaccinating against HIV-1 -
                                                              Luciferase; cell death.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present invention describes a composition (I) comprising
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim
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                                                                                                             Protease peptide
                                                                                                                                                                              AAE19118;
                                                                                                                                                                                                           AAE19118 standard; peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                              21-MAY-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           invention
                                                                                                                                                                                                                                                                                             1 KARVLAEA 8
                                                                                                                                                                                                                                                                                                              2 KARVLAEA 9
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Celis E,
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                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                              enzyme;
                                                                                                                                             (first entry)
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                                                                                                                                                                                                                                                                                                                                         100.0%; Score 35;
100.0%; Pred. No.
                                                                             protease; cell growth; apoptosis; therapeutic;
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7.8e+05;
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WO200206458-A2 Unidentified

17-JUL-2001; 2001WO-US22478

24-JAN-2002

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RESULT 15
AAU75795
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                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                    Gag protein; antiviral; nucleic acid construct; viral protease; protease recognition site; PRS; viral drug resistance; HIV; human immunodeficiency virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New purified luciferase polypeptide, useful for identifying protease activity modulators, comprises recognition site cleavable by protease, where cleavage of polypeptide results in decreased luciferase activity
              W0200210430-A2
                                                            Cleavage-site
                                                                                                        Human immunodeficiency
                                                                                                                                                                                                Human immunodeficiency virus Gag protein protease cleavage sequence
                                                                                                                                                                                                                                     08-MAY-2002
                                                                                                                                                                                                                                                                   AAU75795;
                                                                                                                                                                                                                                                                                               AAU75795 standard; Peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
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                                                             Location/Qualifiers
                                             /label= HIV_protease_cleavage_site
                                                                                                         virus
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Search completed: March 13, 2003, 18:49:14 Job time: 27.5455 secs

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                                                                                                                                                                                             cc and a protesse recognition site (PRS) cleavable by a virally encoded contended, where cleavage of the PRS leads to a detectable signal. The nucleic acid construct of the invention is useful for uncovering consecules having antiviral activity or for determining viral drug cresistance and the chimeric peptide is also useful for detecting the presence of a virus in a cell. Other uses of the invention are detecting the presence of viral infection. The nucleic acid construct is useful for construct is useful for the invention enables screening of molecules in an easy and rapid manner can allows efficient detection of the presence of viral particles within cells. The construct is specific, sensitive and construct is particles within cells. The construct is specific, sensitive and construct is particles within cells. The construct is specific, sensitive and consectivity in the absence of human consection of the presence of viral particles. When the construct is specific viral strain isolates even under low viral load conditions. When used for phenotypic testing of HIV drug resistance it delivers accurate cresuits within 24 hours. The present amino acid sequence represents one of several (AAU75794-AAU75798) HIV Gag protein protease cleavage
                                                                            Query Match
Best Local S
Matches 8
                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The chimeric polypeptide comprises a first polypeptide sequence, a second polypeptide sequence translationally fused to the first sequence,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present invention relates to a new nucleic acid construct that comprises a polynucleotide cassette encoding a chimeric polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New nucleic acid construct for detecting anti-viral drugs, comprises polynuclectide cassette encoding a chimeric polypeptide with two polypeptide sequences and a protease recognition site cleavable by a virally encoded protease.
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                                                                                                 Score 35;
Pred. No.
                                                                                Mismatches
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Perfect score:
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Maximum Match 100%
Listing first 45 summaries
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 Issued_Patents_AA:*
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                                                                                                                                                                                                                                                                                                                                                                                                                                       /cgn2_6/ptodata/2/1aa/5A_COMB.pep:*
/cgn2_6/ptodata/2/1aa/5B_COMB.pep:*
/cgn2_6/ptodata/2/1aa/6A_COMB.pep:*
/cgn2_6/ptodata/2/1aa/6B_COMB.pep:*
/cgn2_6/ptodata/2/1aa/B_COMB.pep:*
/cgn2_6/ptodata/2/1aa/Backfiles1.pep:*
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                    US-08-792-553-4
US-09-053-941-15
US-09-817-413-15
US-09-817-43-76
US-08-460-6028-76
US-08-460-6028-76
US-08-465-2178-76
US-08-465-2178-76
US-08-465-2178-76
US-08-465-2178-77
US-08-460-6028-77
US-08-461-2597-78
US-08-461-2597-77
US-08-463-9668-77
US-08-463-9688-78
US-08-463-9688-78
US-08-463-9688-78
US-08-463-9688-79
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                                                                                                                                                                                     Sequence 4, A
Sequence 15,
Sequence 15,
Sequence 21,
Sequence 76,
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ALIGNMENTS

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Patent No. 45981200
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOTWARE: Patentin Release #1.0, Version #1.25
SOTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/792,553
FILING DATE: 31-JAN-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Lisa A. Halle, Ph.D.
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 07257/041001/UC 96-160-2
                                                                                                                    Query Match
                                                                                 Matches
                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-678-5070
TELEPAX: 619-678-5099
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                              LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Tsien, Roger Y.
APPLICANT: Heim, Roger
TITLE OF INVENTION: Tandem
NUMBER OF SEQUENCES: 25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: 4225 Ex
CITY: La Jolla
STATE: Californ
COUNTRY: USA
2 KARVLAEÅ Å9
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es 8; Conserv
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                                                                              79.5%; Score 35; DB 2; larity 100.0%; Pred. No. 0.36; Conservative 0; Mismatches
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Gaps

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -Sequence 15, Application US/09817413
    Patent No. 6436648
                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQ ID NOS: 25
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQ ID NOS: 25
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 15
Sequence 21, Application US/09147208
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Matches 8; Conserv
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APPLICANT: KOPROWSKI, HILARY
TITLE OF INVENTION: CHIMERIC VIRAL PROTEINS
FILE REFERENCE: Chimeric Viral Proteins
FILE REFERENCE: Chimeric Viral Proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: KOPROWSKI, HILARY
TITLE OF INVENTION: CHIMERIC VIRAL PROTEINS
FILE REFERENCE: Chimeric Viral Proteins
CURRENT APPLICATION NUMBER: US/09/817,413
CURRENT FILING DATE: 2001-03-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/09/053, S
CURRENT FILING DATE: 1998-04-02
EARLIER APPLICATION NUMBER: 60/043,380
EARLIER FILING DATE: 1999-04-03
                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: 60/043,380 PRIOR FILING DATE: 1999-04-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: SRINIVISAN, ALGARSAMY APPLICANT: KOPROWSKI, HILARY
                                                                                                                                                                                                                                                                                          ORGANISM: Human immunodeficiency virus type PUBLICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Human immunodeficiency virus type PUBLICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                          LENGTH: 10
TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           JOURNAL: Meth. Enzymol. VOLUME: 38 PAGES: 299-DATE: 1974
                                                                                                2 KARVLAEA 9
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Pred. No.
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Pred. No.
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0.36;
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TELEPHONE: (416) 364-7311
TELEFAX: (416) 361-1398
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: SIA, Ch
APPLICANT: CHONG,
APPLICANT: KLEIN,
                                                                                                                                                                                                                                                                                                                                                                                          Sequence 76, Application US/08257528B Patent No. 5639854
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GENERAL INFORMATION:
                                                                    COUNTRY: CANADA
ZIP: M5G 1R7
ZIP: M5G 1R7
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRANDEDNESS:
TOPOLOGY: lin
MOLECULE TYPE:
SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/257,528B
FILING DATE: 09-JUN-1994
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA: APPLICATION NUMBER: US//9/147,208 FILING DATE: 02-MAR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 71
CORRESPONDENCE ADDRESS:
ADDRESSEE: BERESKIN & PARR
STREET: 40 King Street West
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: Tandem Synthetic HIV-1 Peptides NUMBER OF SEQUENCES: 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION:
                                                                                                                                                                                                             STREET: Suite
CITY: Toronto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Rudolph, John R. REGISTRATION NUMBER: 38 REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
les 8; Conserv
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CITY: Toronto
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M5H 3Y2
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Suite 701, 330 University Avenue
                                                                                                                                                                                                                                                                                                                                      CHONG, Pele
                                                                                                                                                                                                                                                                                                                         KLEIN, Michel H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
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linear
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SYSTEM: PC-DOS/MS-DOS
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100.08; F1
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ATTORNEY/AGENT INFORMATION:

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Query Match
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Query Match
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COMPUTER READABLE FORM:
MEDIUM TYPE: Florr
                                                                                                                                                                         APPLICATION NUMBER: 08/257,528
FILING DATE: 09-JUN-1994
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/073,378
FILING DATE: 09-JUN-1993
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: STEWART, MICHAEL 1.
REGISTRATION NUMBER: 24,973
REGISTRATION NUMBER: 24,973
                                                                                            TELEFAX: (416) 595-1163
INFORMATION FOR SEQ ID NO: 76:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
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SEQUENCE CHARACTERISTICS:
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LACTERISTICS:
LYPE: amino acid
STRANDEDNESS: s;
TOPOLOGY:
157-52°
                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                        TELEPHONE: (416) 595-1155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: 10
TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET: Suite 70
CITY: Toronto
STATE: Ontario
                                                      TYPE: amino acid
STRANDEDNESS: si
                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/0 FILING DATE: 02-JUN-1995 CLASSIFICATION: 424
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                                                                                   ENGTH:
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                                                                                15 amino acids
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KLEIN, Michel H.
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NO: 76:
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 79.5%;
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Score 35;
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DB 1;
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Length 15;
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RESULT 8
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                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: 08/257
FILING DATE: 09-JUN-1994
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/07:
FILING DATE: 09-JUN-1993
CLASSIFICATION: 424
                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 05-JUN-1335
FILING DATE: 05-JUN-1335
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: 08/257,528
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: STEWART, MICHAEL I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES:
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3 KARVLAEA 10
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3 KARVLAEA 10
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                                                                                                                                                                                                        STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038-487 MIS:jb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OPERATING SYSTEM:
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Suite 701, 330 University Avenue
                                                                                                                                                                                                                                                                          :: (416) 595-1155
(416) 595-1177
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KLEIN, Michel H.
                                                                                                                 Conservative
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IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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) 595-1163
NO: 76:
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                                                                                                                               79.5%; Score 35; 100.0%; Pred. No.
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0; Mismatches
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Sequence 76, Application US/0846
Patent No. 5800822
GENERAL INFORMATION:
APPLICANT: SIA, Charles D.Y.
APPLICANT: CHONG, Pele

76, Application US/08465217A o. 5800822

CURRENT APPLICATION DATA:

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Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                Sequence 76, Applicate Patent No. 5817754 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: (416) 595-1155
INFORMATION FOR SEQ ID NO: 76:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acids
STRANDEDNESS: Single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 05-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION UNMBER: 08/257,528
FILING DATE: 09-JUN-1994
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION UNMBER: 08/073,378
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                               NUMBER OF SEQUENCES: 1:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                  APPLICANT: SIA, Charles D.Y.
APPLICANT: CHONG, Pele
APPLICANT: KLEIN, Michel H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: STEWART, MICHAEL I.
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 10
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                       TITLE OF INVENTION
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
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FITLE OF INVENTION: Tandem
                                                                                                    COUNTRY:
                                                                                                                       STATE:
                                                                                                                                    CITY: Toronto
                                                                                                                                                     STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC COMPACTIVE OPERATING SYSTEM: PC-DOS/MS-DOS
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CITY: Toronto
                                                                                                                                                                    ADDRESSEE:
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CLASSIFICATION: 424
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5817754
                                                                                                                     Ontario
                                                                                                                                              E: Sim & McBurney
Suite 701, 330 University Avenue
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                                                                                                    Canada
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  79.5%; Score 35; ilarity 100.0%; Pred. No. Conservative 0; Mismatc
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                                                                                                                                                                                                                  Tandem Synthetic HIV-1 Peptides
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US-08-462-507A-76
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Best Local Similarity
Matches 8; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                            COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PATENTIA RELEASE #1.0,

CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: (416) 595-11:
TELEFAX: (416) 595-1163
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
                                         APPLICATION NUMBER: 08/257
FILING DATE: 09/UN-1994
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/073
FILING DATE: 09-UN-1993
CLASSIFICATION: 424
                                                                                                                                                         APPLICATION NUMBER: US/01
FILING DATE: 05-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
STRANDEDNESS: single
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REFERENCE/DOCKET NUMBER: 10
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: SIA, Charles D.Y.
APPLICANT: CHONG, Pele
APPLICANT: KLEIN, Michel H.
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/073,378
FILING DATE: 09-JUN-1993
                         ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: Tandem Synthetic HIV-1 Peptides NUMBER OF SEQUENCES: 101
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NAME: STEWART, MICHAEL I
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PRIOR APPLICATION DATA:
08/257,528
                                                                                                                                                                                                                                                                                                                                COUNTRY: Canada
ZIP: M5G 1R7
                                                                                                                                                                                                                                                                                                                                                                               STREET: Suite
CITY: Toronto
REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: FILING DATE: 05-JU
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION:
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Suite 701, 330 University Avenue
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                                                                                                                                               08/257,528
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                                                                             08/073,378
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US-08-462-507A-76
                                                              US-08-467-881A-76
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US-08-467-881A-76
 Query Match 79.5%; Sometime 8; Conservative 0;
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FILING DATE: 09-JUN-1993

CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:
NAME: STEWART, MICHAEL I.
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                                                                                                     TELEFAX: (416) 595-1163
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
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INFORMATION FOR SEQ ID NO: 76:
                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 424
PRIOR APPLICATION DATA:
08/257,528
                                                                                                                                                                                          REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 10
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                            CLASSIFICATION: 424
CRASSIFICATION DATA:
PRIOR APPLICATION NUMBER: 08/073,378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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LENGTH: 15 amino acids
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CORRESPONDENCE ADDRESS:
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                                                                                        STRANDEDNESS:
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STRANDEDNESS: sir
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les 8; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER:
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KLEIN, Michel H.
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 Score 35; DB 2; 
; Pred. No. 0.55; 
0; Mismatches
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Pred. No.
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US-08-257-528B-47
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US-08-460-602A-47
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Best Local Similarity
Matches 8; Conserv
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INFORMATION FOR SEQ ID NO: 4
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                               GENERAL INFORMATION:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 595-1155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/257,528B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                               APPLICANT: SIA, Charles D.Y.
APPLICANT: CHONG, Pele
APPLICANT: KLEIN, Michel H.
                                                                                       NUMBER OF SEQUENCES: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION: NAME: STEWART, MICHAEL I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
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                                                                                                                   TITLE OF INVENTION:
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                                        STREET: Suite
CITY: Toronto
                                                                                                                                                                                                                                                                                                                                                                                                                                     STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/0 FILING DATE: 09-JUN-1994 CLASSIFICATION: 424
               COUNTRY:
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amino acid
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Suite 701, 330 University Avenue
                                                         Suite 701, 330 University Avenue
               Canada
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KLEIN, Michel H.
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100.0%; Pr
                                                                                                                    Tandem Synthetic HIV-1 Peptides
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Pred. No
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1038-336 MIS:jb
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                                                  SOFTMARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION UNMERR: US/08/463,966A
FILING DATE: 05-UN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/257,528
FILING DATE: 09-UN-1994
                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 101
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sim & McBurney
STREET: Suite 701, 330 University Avenue
                                                                                                                                                                                                       COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: SIA, Charles D.Y.
APPLICANT: CHONG, Pele
APPLICANT: KLEIN, Michel H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 32 amino acids
TYPE: amino acid
STRANDEDNESS: single
                  PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION: TELEPHONE: (416) 595-1155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: 08/0 FILING DATE: 09-JUN-1993 CLASSIFICATION: 424 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 424
PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                               ZIP: M5G 1R7
                                        CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                  CITY: Toronto
STATE: Ontario
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Polonia
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038-450 MIS:jb
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/08/460,602A FILING DATE: 02-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: 08/2
FILING DATE: 09-JUN-1994
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08/073,378
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US-08-465-217A-47; Sequence 47, Ap; Patent No. 5800
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Best Local Similarity 100
Matches 8; Conservative
                                                                       TELEFAX: (416) 595-1163 INFORMATION FOR SEQ ID NO:
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TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: line

463-060
SEQUENCE CHARACTERISTICS:
LENGTH: 32 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                      REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038-486 MIS:jb
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTMARE: Patentin Release #1.0, Ve
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/465,217A
FILING DATE: 05-JUN-1995
CLASSIFICATION: 424
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ATTORNEY/AGENT INFORMATION:
NAME: STEWART, MICHAEL I.
                                                                                                                                                                                                                                                                    CLASSIFICATION: 424
PRIOR APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 595-1155
                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/257,528
FILING DATE: 09-JUN-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: SIA, Charles D.Y.
APPLICANT: CHONG, Pele
APPLICANT: KLEIN, Michel H.
TITLE OF INVENTION: Tandem S
NUMBER OF SEQUENCES: 101
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NAME: STEWART, MICHAEL I.
REGISTRATION NUMBER: 24,973
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET: Suite
CITY: Toronto
                                                                                                         TELEPHONE:
                                                                                                                                                                                                                                   APPLICATION NUMBER: 08/0 FILING DATE: 09-JUN-1993
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US-08-465-217A-47

Query Match 79.5%; Score 35; DB 1; Length 32;
Best Local Similarity 100.0%; Pred. No. 1.2;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 KARVLAEA 9

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Db 3 KARVLAEA 10

Search completed: March 13, 2003, 18:53:52

Job time: 9.90909 secs
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Result
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  Pred. No: is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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Q15608 homo sapien
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Q918u9 brachydanio
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CONTRAIN-GSS1 / DSM 4299 / JCM 9571;

CONTRAIN-GSM 971, Makino S.-I., Higuchi S.,

CONTRAIN-GSS1 / Makino S.-I., Makino S.-I., Makino S.-I., Higuchi S.,

CONTRAIN-GSS1 / Makino S.-I., Maki
                                                                                                                                       Matches
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Best Local
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O978R7; O1-OCT-2001 (TrEMBLrel. 18, Created)

O1-OCT-2001 (TrEMBLrel. 18, Last sequence update)

O1-MAR-2002 (TrEMBLrel. 20, Last annotation update)

N-terminal acetyltransferase complex subunit.

TV1348 OR TVG1394372.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Thermoplasma volcanium.

Archaea: Euryarchaeota; Thermoplasmata; Thermoplasmatales; Thermoplasmataceae; Thermoplasma.
                                                                                                                                                                                                                                                                        SEQUENCE
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      49
1 ERAEQQRLKSQD 12
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49 ERAEQERIKSLD 60
                                                                                                                                    Similarity
9; Conserv
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77 AA; 20436 MW;
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75.0%;
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K., Kawamoto
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01-MAR-2001 (TrEMBLrel. 16, L
01-MAR-2002 (TrEMBLrel. 20, L
Hypothetical protein Ta0277.
TA0277.
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  Q90Y46
Q90Y46;
Q1-DEC-2001
Q1-DEC-2001
                                                                                                                                                                                                                                                                                                                                                 Jin J.-P., Biesladecki B.;
"Mutant turkey cardiac troponin T.";
submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases
EMBL; AF274301; AAK58685.1; -
InterPro; IPR001978; Troponin.
Pfam; PF00992; Troponin; 1.
SEQUENCE 281 AA; 33651 MW; 7BF0B960E7674718 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
STRAIN-DSM 1728;
MEDLINE-20479972; PubMed-11029001;
Ruepp A., Graml W., Santos-Martinez M.-L., Koretke K.K., Volker C.,
Mewes H.-W., Frishman D., Stocker S., Lupas A.N., Baumeister W.;
"The genome sequence of the thermoacidophilic scavenger Thermoplasma acidophilum.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Meleagris gallopavo (Common turkey).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Meleagrididae; Meleag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nature 407:508-513(2000).

EMBL: AL445063; CAC11422.1; -.

InterPro; IPR000182; GCN5acetyltransf.

Pfam: PF00583; Acetyltransf; 1.

Hypothetical protein; Complete proteome.

SEQUENCE 179 AA; 20547 MW; 2B12B57CE83C6FDC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Thermoplasma acidophilum.
Archaea; Euryarchaeota; Thermoplasmata;
Thermoplasmataceae; Thermoplasma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q9HLF1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=9103;
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8; Conserv
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9; Conser
  (TrEMBLrel.
                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                   Conservative
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72.7%;
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Last sequence update)
Last annotation updat
Created)
Last sequence update)
                                                                                                                                                                                                                                                                 Score 44; DB
Pred. No. 6.5;
3; Mismatches
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Pred. No.
                                                                    PRT;
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1.9;
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on update)
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Matches
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Best Local S
Matches 8
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"Mutant turkey cardiac troponin T.
Submitted (JUL-2000) to the EMBL/(
EMBL; AY005139; AAG23714.1; -.

InterPro; IPR001978; Troponin.
Pfam; PF00992; Troponin; 1.

SEQUENCE 293 AA; 34892 MW; 7D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     090YN7;
01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Cardiac troponin T isoform.
Meleagris gallopavo (Common turkey).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Galliformes; Meleagrididae; Meleagri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; (Actinopterygii; Neop)
Actinopterygii; Neop)
Cyprinidae; Danio.
NCBI_TaxID=7955;
                                                                                                                                                                                             01-MAY-2000 (TrEMBLrel. 13, 01-MAY-2000 (TrEMBLrel. 13, 01-MAR-2002 (TrEMBLrel. 20,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "The Zebrafish silent heart Mutation Disrupts cell-Autonomously Reduces Cardiac Troponin T submitted (JUN-2000) to the EMBL/GenBank/DDBJ EMBL; AF282384; AAL06279.1; - ZFIN; ZDB-GENE-000626-1; tnnf2. InterPro; IPR001978; Troponin. pfam; pF00992; Troponin; 1. SEQUENCE 282 AA; 33986 MW; EE7450B0A50B1D2
                                 Deinococcus radiodurans.
Bacteria; Thermus/Deinococcus
                                                                                                                                                                                                                                                                                                                             Q9RYG4;
                                                                                                                                                                                                                                                                                                                                                              Q9RYG4
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Eukaryota; Metazoa; Chordata;
Actinopterygil; Neopterygil; T
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    Deinococcaceae;
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                                                                                                                                                        Methyl-accepting
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||||||::|:
| ERAEQQRIRSE 148
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ERAEQQRIRSE
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        Deinococcus.
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-related protein.
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Pred. No.
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; Craniata; Vertebrata; Euteleostomi;
Teleostei; Ostariophysi; Cypriniformes;
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                                         group;
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6.5;
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                                             Deinococcales;
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SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.";
Science 286:1571-1577(1999).
EMBL; AE001863; AAF12432.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=20036896; PubMed=10567266; White O., Eisen J.A., Heidelberg J.F., Hickey E.K., Peterson J.D., White O., Eisen J.A., Heidelberg J.F., Hickey E.K., Peterson D.L., Dodson R.J., Haft D.H., Gwinn M.L., Nelson W.C., Richardson D.L., Dodson R.J., Lam P., Jang L., Pamphile W., Crosby M., Shen M., Vamathevan J.J., Lam P., McDonald L., Utterback T., Zalewski C., Makarova K.S., Aravind L., Daly M.J., Minton K.W., Fleischmann R.D., Ketchum K.A., Nelson K.E., Salzberg S., Smith H.O., Venter J.C.,
                                                                                                                                                                                                                                                                                                                                                                                             Townsend P.J., Barton P.J.R., Yacoub M.H., F Molecular cloning of human cardiac trponin developing and failing heart.", J. Mol. Cell. Cardiol. 27:2223-2236(1995). EMBL; X79859; CAA56239.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-NOV-1996 (TremBLrel. 01, 01-NOV-1996 (TremBLrel. 01, 01-JUN-2002 (TremBLrel. 21, Troponin T (Fragment).
  Q9Z0X5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa;
Mammalia; Eutheria;
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InterPro; IPR003660; HAMP.
Pfam; PF00672; HAMP; 1.
Pfam; PF00015; MCPsignal; 1.
SMART; SM00304; HAMP; 2.
                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
MEDLINE-96129582; PubMed-8576938;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID-9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens (Human)
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TIGR; DRA0353; -.
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| | | | | | | | ::::
| ERAEQQRIRNE
                                                                                                                                                                                                                                                                                                                              Pro; IPR001978; Troponin. Pr00992; Troponin; 1. ER 175 175
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SM00283; MA; 1.
                                                                                                                                                                                                           7; Conserv
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9; Conserv
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756 AA;
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  PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chordata;
                                                                                                                                                                                                                                                                                                     20918 MW;
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Pred. No.
                                                                                                                                                                                                                                 Score 41; DB
Pred. No. 14;
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  PRT;
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  177
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25;
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n T isoforms: expression
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RX KRAWai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,

RA Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,

RA Kadota K., Matsuda H.A., Sahburner M., Batalov S., Casswant T.,

RA Kadota K., Matsuda H.A., Sahburner M., Batalov S., Casswant T.,

RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,

RA Kuehl P., Lewis S., Matsuo Y., Nikaldo I., Pesole G., Quackenbush J.,

RA Kuehl P., Lewis S., Matsuo Y., Nikaldo I., Pesole G., Quackenbush J.,

RA Schrimi L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,

RA Schrimi L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,

RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,

RA Blake J., Boffelli D., Hofmann M., Hume D.A., Kaniya M., Lee N.H.,

RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kaniya M., Lee N.H.,

RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,

RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,

Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,

RA Wanshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,

Wanshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
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Best Local
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O9D1S7;
01-JUN-2001 (TremBLrel. 17, Created)
01-JUN-2001 (TremBLrel. 17, Last sequence update)
01-JUN-2001 (TremBLrel. 17, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    O9ZOX5;
01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Troponin T (Fragment).
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Am. J. Physiol.
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
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Submitted (CCT-1998) to the EM
EMBL; AF099071; AAD16291.1; -.
InterPro; IPR001978; Troponin.
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MEDLINE-99345814; PubMed-10409222;
Preisig-Muller R., Mederos y Schnitzler M.,
"Separation of cardiomyocytes and coronary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cavia porcellus (Guinea pig).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eut
Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae;
Hayashizaki Y.; 
"Functional annotation of a Nature 409:685-690(2001).
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7; Conserv
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hysiol. 277:H413-H416(1999)
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177
177 AA;
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                               full-length
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Pred. No.
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Sciurognathi; Muridae;
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14;
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RESULT 11
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ID 09TS3
AC 09TS3
AC 09TS3
DT 01-MA
DT 01-JU
DE Tropo
OS OTYCT
OC Eukar
OC Mammab
OX NCBI_
RN [1]
RP SEQUE
RX MEDLJ
RA Pan E
RT Deta
RT beta
DR Inten
DR Inten
DR Pfam;
SQ SEQUI
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Xu Y., He J., Wang X., Lim T.M., Gong Z.;
"Asynchronous activation of 10 muscle-specific protein (MSP) genes during zebrafish somitogenesis.";
Dev. Dyn. 219:201-218(2000).
EMBL: AF180889; AAF78472.1; -.
ZFIN; ZDB-GENE-000322-3; tnnt.
InterPro; IPR001978; Troponin.
Pfam; PF00992; Troponin; 1.
                    MEDLINE-93054628; PubMed-1429653;
Pan B.S., Potter J.D.;
"Two genetically expressed troponin T fragments beta isoforms exhibit functional differences.";
J. Biol. Chem. 267:23052-23056(1992).
InterPro; IPR001978; Troponin.
Pfam; PF00992; Troponin; 1.
                                                                                                                                                                                                                                                                 Oryctolagus cuniculus (Rabbit).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
                                                                                                                                                                                                                                                                                                                                                   01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
Troponin T alpha isoform.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Brachydanio rerio (Zebrafish) (Zebra danio).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Acthopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniform
Cyprinidae; Danio.
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01-OCT-2000 (TrEMBLrel. 15, Last sequence up
01-DEC-2001 (TrEMBLrel. 19, Last annotation
First skeletal muscle troponin T.
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01-OCT-2000
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     SEQUENCE
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AA; 27786 MW;
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  27809 MW;
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4; Mismatches
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Q9TS31;
Q9TS31;
01-MAY-2000;
01-MAY-2000;
01-JUN-2001;
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                                                                                                      Townsend P.J., Barton P.J.R., Yacoub M.H., Farza H.;

Molecular cloning of human cardiac trponin T isofors
developing and failing heart.",
J. Mol. Cell. Cardiol. 27:2223-2236(1995).
EMBL; X79861; CAA56240.1;
InterPro; IPR001978; Troponin.
Pfam; pP00992; Troponin; 1.

NON_TER 250 250
                                                                                                                                                                                                                                                                                  TISSUE-HEART MUSCLE;
MEDLINE-96129582; PubMed-8576938;
                                                                                      SEQUENCE
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J. Biol. Chem. 267:23055-23056(1992).
InterProj. IPR001978; Troponin.
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Pan B.S., Potter J.D.;
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Similarity 7; Conserv
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  Conservative
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AA; 29683 MW;
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                                                                                      30151 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        090Z47 PRELIMINARY; PRT; 271 AA.
090Z47; Q90Z46; 035575; 035576; 035578; 035580;
035281; 035582; 035583; 035584; 035585; p97456;
01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
Troponin T, fast skeletal muscle isoforms.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cardiomyopathy.";

Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases

EMBL; AY005143; AA623718.1; -

Interpro; IPR001978; Troponin.

Pfam; PF00992; Troponin; 1.

SEQUENCE 270 AA; 32339 MW; 316105372CACC80D CRC64;
Mammi. Genome 8:346-348(1997).

-!- FUNCTION: TROPONIN T IS THE TROPOMYOSIN-BINDING SUBUNIT OF TROPONIN, THE THIN FILAMENT REGULATORY COMPLEX WHICH CONFERS CALCIUM-SENSITIVITY TO STRIATED MUSCLE ACTOMYOSIN ATPASE ACTIVIBY SIMILARITY).

-!- ALTERNATIVE PRODUCTS: AT LEAST 13 ISOFORMS; A1E17 (SHOWN HERE), A2E17, A3E17, A4E17, A5E17, A6E17, B1E16, B2E17, B2E16,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING. STRAIN-129/SVJ; TISSUE-SKELETAL MUSCLE; MEDLINE-97390134; PubMed-9249073; Wang J., Jin J.-P.; Wang J., Jin J.-P.; Trimary structure and developmental acidic to the structure and the 
                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=97262102; PubMed=9107680;
Koch A., Juan T.S.-C., Jenkins N.A.,
McNiece I.K., Fletcher F.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Primary structure and developmental acidic to basic transition alternatively spliced mouse fast skeletal muscle troponin T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TNNT3.
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                                                                                                                                                                                                                                                                                               troponin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gene 193:105-114(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID-10090;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=9615;
                                                                                                                                                                                                                                                                                               "cDNA cloning and chromosomal mapping of
troponin T.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 isoforms."
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
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                                                                                                                                                                                                                                                                                                                                     fast skeletal muscle
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                                                                                                                                                                                                                                                                                                                           InterPro;
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115
                1 ERAEQQRLKSQ 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           B3E17/PTROPT, B3E16, B4E17 AND B4E16; ARE PRODUCED BY ALTERNATIVE SPLICING: ISOFORMS ALE17, A2E17, A3E17, A4E17, A5E17 AND A6E17 ARE ACIDIC WHILE ISOFORMS B1E16, B2E17, B2E16, B3E17, B3E16, B4E17 AND 184E16 ARE BASIC: EXPRESSED PREDOMINANTLY IN SKELETAL MUSCLE: DEVELOPMENTAL STAGE: EMBRYO AND NEONATE EXPRESS PREDOMINANTLY ONE ACIDIC ISOFORMS WHILE ALL ADULT ISOFORMS ARE BASIC: ONLY ONE
                                                                                                                                                                                                                                                                                                                                                     ISOFORM, B2E17, IS FOUND IN BOTH EMBRYO/NEONATE AND ADULT. TRANSITION FROM HIGH TO LOW MOLECULAR WEIGHT ISOFORMS IS A DURING POSTNATAL DEVELOPMENT.
ERAEQQRIRAE 125
                                                                                                                                                                                                                                                                                                                                               U77779; AAB39743.1;
                                                                                                                                                                                                                                                                                                         protein; Alternative
                                    Similarity 7; Conser
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271
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                                                                                                 AND ISOFORM BEE16).

AND ISOFORM BEE17, ISOFORM A5E17, ISOFORM BEE17 ISOFORM BEE16).

ISOFORM BEE17 AND ISOFORM BEE16).

TILRSRIDOAQKH -> MTVRARVEMLAKF (IN ISOFORM B1E16, ISOFORM BEE16, ISOFORM BEE16).

B 3E16 AND ISOFORM B4E16).

P -> R (IN AAB67283, AAB67284, AAB67285, AAB67286, AAB67287, AAB67288 AND
                                   Score 41; DB
Pred. No. 21;
4; Mismatches
                                                                                                                                                                                                                                                                                                          splicing; Multigene family;
                                                                                 AAB67289)
A -> T (I)
                                                                                                                                                                                                            B4E16)
                                                                                                                                                                                                                    AND ISOFORM B2E16).
MISSING (IN ISOFORM
                                                                                                                                                                                                                                                  B4E16)
                                                                                                                                                                                                                                                         BY SIMILARITY.
PHOSPHORYLATION (BY CK2) (BY SIMILARITY).
MISSING (IN ISOFORM A4E17, ISOFORM B3E17,
ISOFORM B3E16, ISOFORM B4E17 AND ISOFORM
                                                                                                                                                                                 AND ISOFORM
                                                                                                                                                                                                     MISSING
                                                                                                                                                                                                                                         MISSING (IN ISOFORM A3E17,
                                                                        -> T (IN REF. 2).
D2CBB544B8C7953F
                                                                                                                                                                                                   (IN ISOFORM A2E17,
                                                       DB 11;
                                                                                                                                                                                          A6E17).
                                                                                                                                                                                ISOFORM B1E16,
                                    0
                                                     Length 271;
                                                                          CRC64;
                                                                                                                                                                                                                      B4E17
                                                                                                     , AAB67284, AAB67285,
AAB67288 AND
                                    Indels
                                                                                                                                                                                                                       AND ISOFORM
                                                                                                                                                                                                   ISOFORM A4E17
                                                                                                                                                                                                                                         ISOFORM B2E17
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                                                                                                                                                                                 ISOFORM B3E17
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Result
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      Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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Gapop 10.0 , Gapext 0.5
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  SwissProt_40:*
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TRT3_HUMAN
TRT3_HUMAN
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CAFA_HUMAN
TMI_XENLA
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TRT2_CHICK
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P02642 gallus gall
P06398 coturnix co
P45378 homo sapien
  P450751
P507753
P507752
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P0099c8
P13805
P033495
P29556
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P13789
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0 gallus gall
1 oryctolagus
9 bos taurus
1 ovis aries
9 homo sapien
                                                                                                                                                                                                                                             5 rattus norv
8 streptococc
5 homo sapien
9 drosophila
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Q40505	FL2_TOBAC	щ.	416	54.8	ω.	44
0405	FL1_TOBAC	ب	413	54.8	34	43
P490	PAM_STRPY	ᆫ	388	54.8	34	42
0705	DIA2_MOUSE	ᆫ	349	54.8	34	41
P786	SEPA_EMENI	ب	1790	56.5	35	40
P535	RLR1_YEAST	Н	1597	56.5	<u>ა</u>	39
P331	CADL_CHICK	Н	732	56.5	35	38
2608	P137_MOUSE	Н	656	56.5	35	37
P183	DREB_CHICK	Н	652	56.5	35	36
Q144	P137_HUMAN	<u> </u>	649	56.5	ω Çi	35
P2955	HMAA_DROME	Н	590	56.5	35	34

ALIGNMENTS

RRRRRR	R R P	RRR	P R 7	3 2 2 2 3	R R	RRX	R R R	R	R R	R R	R R	R RT	RT A	R. ₹	RR	288	8 8 5	DE DE		D I	147	RESULT FCE2_H ID F
. ⊢ (0 5< k)	Biochem. J. 286:819-824(1992). [5] ALTERNATIVE SPLICING.	.U., Magnenat E., Aubonney N., Bonne characterization of natural and rec	Turcatti G., Graber P., Pochon S., Regame)	6:109-114(1987).	r E., Frost H., Delespesse G.; and expression of the cDNA coding for a human lymphocyte	454; F	Cell 47:657-665(1986). [3] SPONENCE FROM N A	"Motecutar structure or numan tymphocyte receptor for immunogiobulin	Kaisho T., Uchibayashi N., Hardy R.R., Hi , Sakiyama F., Suemura M., Kishimoto T.;	1737; PubMed-2877743; Inui S., Sato R., Barsumian	NCE FROM N.A.	cDNA with animal lectins."; Natl. Acad. Sci. U.S.A. 84:819-823(1987).	lymphocyt	Ikuta K., Takami M., Kim C.W., Honjo T., Miyoshi T., Tagaya Y.,	30.40	malla; Eutheria; Primates; Catarrhini; Hominidae; I_TaxID-9606;	MOCHANOS. Chordata. Craniata. Vortobrata. E GEBr.	r).	LOW affinity immunoglobulin epsilon FC receptor (Lymphocyte IgE receptor) (FC-epsilon-RII) (CD23) (BLAST-2) (Immunoglobulin E-binding	(Rel. 41, Last sequence update)	06, Created)	1 5

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EMBL; M15059; AAA52434.1; -.
EMBL; M14766; AAA52435.1; -.
EMBL; X04772; CAA28465.1; -.
EMBL; M23562; AAA52433.1; -.
PIR; A26067; LNHUER.
PIR; A26164, A26164.
PIR; A26589; A26589.
PIR; A31924; A31924.
PIR; J10132, J10132.
REPEAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for comentities requires a license agreement (See http://www.isb-sib.ch/anor send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Protein Sci. 5:240-247(1996).

-IP FUNCTION: THIS RECEPTOR HAS ESSENTIAL ROLES IN THE REGULATION OF IGE PRODUCTION AND IN THE DIFFERENTIATION OF B-CELLS (IT A B-CELL-SPECIFIC ANTIGEN).

-IP SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. ALSO EXISTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Padlan E.A., Helm B.A.;
Modeling of the lectin-homology
"finity Fc epsilon receptor (Fc
Receptor 3:325-341(1993).
[7]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bajorath J., Aruffo A.;
"Structure based modeling of the ligand binding coell surface receptor CD23 and comparison of two derived molecular models.";
                                                                                                                                                                          CHAIN
                                                                                                                                                                                                                                      InterPro; IPR001304; Lect Pfam; PF00059; lectin_c; SMART; SM00034; CLECT; 1
                                                                                                                                                                                                                                                                          Genew; HGNC:3612; FCER2.
MIM; 151445;
                                                                                                                                                                                                                                                                                                     PDB; 1KJE; 03-APR-96.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3D-STRUCTURE MODELING OF LECTIN DOMAIN. MEDLINE-94191542; PubMed-8142907;
                                                                                                                                 TRANSMEN
                                                                                                                                                DOMAIN
                                                                                                                                                           CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-96276216;
                                                                                                                                                                                     Repeat;
                                                                                                                                                                                                ge-binding
                                                                                                                                                                                                                            PROSITE;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   [6]
3D-STRUCTURE MODELING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MISCELLANEOUS: THERE ARE TWO KINDS OF FC RECEPTORS FOR IGE, WHICH DIFFER IN BOTH STRUCTURE AND FUNCTION: HIGH AFFINITY RECEPTORS ON BASOPHILS AND MAST CELLS AND LOW AFFINITY RECEPTORS ON LYMPHOCYTES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A SOLUBLE EXCRETED FORM.

ALTERNATIVE PRODUCTS: 2 ISOFORMS; A (SHOWN HERE)
PRODUCED BY ALTERNATIVE SPLICING.
PTM: N- AND O-GLYCOSYLATED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SIMILARITY: CONTAINS 1 C-TYPE LECTIN FAMILY DOMAIN. DATABASE: NAME-PROW; NOTE-CD guide CD23 entry; WWW-"http://www.ncbi.nlm.nih.gov/prow/cd/cd23.htm".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AND MONOCYTES.
                                                                                                                                                                                    Lectin;
                                                                                                                                                                                                         PS00615; C_TYPE_LECTIN_1; 1. PS50041; C_TYPE_LECTIN_2; 1.
                                                                                                                                                                                                                                                              IPR001304; Lectin_C.
 48
162
149
69
90
111
160
163
                                                                                                                                                                                                  protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MODELING
                                                                                                                                                                      Signal-anchor; Alternative splicing; 321 MEMBRANE BOUND FORM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LING OF 173-285.
PubMed-8745401;
 321
284
150
150
110
113
131
288
174
                                                                                                                                                                                   Transmembrane; Glycoprotein; Receptor; B-cell; bl-anchor; Alternative splicing; 3D-structure.
             ВХ
                                                                             (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
C-TYPE LECTIN (LONG FORM).
CLEAVAGE.
                                                                                                                            SOLUBLE FORM.
CYTOPLASMIC (POTENTIAL).
SIGNAL-ANCHOR (TYPE-II MEMBRANE
             SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             domains
epsilon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             of the human and RII/CD23).";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IN THE REGULATION
OF B-CELLS (IT I
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                                                                                                                                 PROTEIN)
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TRT 2_CI
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Best Local S
Matches 12
Query Match
Best Local Similarity
                                                                    VARSPLIC
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DISULFID
CARBOHYD
VARSPLIC
CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     and skeletal muscle development.";
Science 226:979-982(1984).
In FUNCTION: TROPONIN T IS THE TROPOMYOSIN-BINDING SUBUNIT OF TROPONIN, THE THIN FILAMENT REGULATORY COMPLEX WHICH CONFERS CALCIUM-SENSITIVITY TO STRIATED MUSCLE ACTOMYOSIN ATPASE ACTIVITY.
I-ALTERNATIVE PRODUCTS: 2 isoforms; 1/Embryonic form (shown here) and 2/Adult form; are produced by alternative splicing.
SIMILARITY: BELONGS TO THE TROPONIN T FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21-JUL-1986 (Rel. 01, Created)
01-AUG-1988 (Rel. 08, Last sequence up
15-JUN-2002 (Rel. 41, Last annotation
Troponin T, cardiac muscle isoforms (3
Gallus gallus (Chicken)
                                                                                                                                         Phosphorylation.
INIT_MET 0
MOD_RES 1
                                                                                                                                                                                                                                                                                  EMBL; M10013; AAA49099.1;
EMBL; K02263; AAA49098.1;
PIR; A03086; TPCHTC.
PIR; A25373; A25373.
                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=85065747; PubMed=6095446; Cooper T.A., Ordahl C.P.; *A single troponin T gene regulated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. (ISOFORMS 1 AND MEDLINE-85289327; PubMed-2993302; Cooper T.A., Ordahl C.P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; (Archosauria; Aves; Neognathae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CHICK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   P02642;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TRT2_CHICK
                                                                                                                                                                                                             Pfam; PF00992; Troponin; 1.
Muscle protein; Alternative
                                                                                                                                                                                                                                                                                                                                                                                                                      entities requires a license agreement (See http://www.isb-sib.ch/announce,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE OF 67-301 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "A single cardiac troponin T gene generates embryonic and adult isoforms via developmentally regulated alternate splicing."; J. Biol. Chem. 260:11140-11148(1985).
                                                                                                                                                                                                                                                       InterPro; IPR001978; Troponin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID-9031;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            96 RAEQQRLKSQDL 107
                                                                                                                                                                                                                                                                                                                                                                                                  send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 RAEQQRLKSQDL
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321 AA;
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36468
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                                                                         X.
                                                                  BY SIMILARITY.
PHOSPHORYLATION (BY CK2)
(BY SIMILARITY).
MISSING (IN ISOFORM 2).
MF85CE1A47F07DD94 CRC64;
                                                                                                                                                                                                             splicing; Multigene family;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         <u>.</u>
Score
Pred.
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Pred. No.
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MEEGQYS -> MNPPSQ (IN ISOFORM B).
N -> T (IN REF. 3).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      F86708C0E6515B87 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 1;
0.0084;
                        DB 1;
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                        Length 301
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RESULT 3
TRT3_COTJA
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Best Local
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Muscle proc.
Phosphorylation.
Phosphorylation.
O
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Ol-JAN-1988 (Rel. 06, Created)
Ol-OCT-1996 (Rel. 34, Last sequence update)
Ol-OCT-1996 (Rel. 41, Last annotation update)
Troponin T, fast skeletal muscle isoforms.
Coturnix coturnix japonica (Japanese quall).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               mammals."
J. Biol.
                                                                                                                                      VARSPLIC
VARSPLIC
                                                                                                                                                                                                                                                                                                                                         EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                      use by non-profit institutions as long modified and this statement is not removed. entities requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-86033836; PubMed-3840482;
Hastligs K.E.M., Bucher E.A., Emerson C.P. Jr.;
"Generation of troponin T isoforms by alternative
avian skeletal muscle. Conserved and divergent fea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
MEDLINE-89308680; PubMed-2745456;
MEDLINE-89308680; PubMed-2745456;
Bucher E.A., de la Brousse F.C., Emerson C.P. Jr.;
"Developmental and muscle-specific regulation of a "Developmental and muscle-specific regulation of a "troponin T isoform expression by mRNA splicing.";
                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                        Pfam;
                                                                                                                                                                                                                                                                                                                         EMBL;
                                                                                                                                                                                                                                                                                                                                                        EMBL;
                                                                                                                                                                                                                                                                                                                                                                        EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     the European Bioinformatics Institute. There are no rest
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This
                                                                                                                                                                                                                                                                                           PIR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE OF 108-252 FROM N.A.
                                                                                                                                                                                                                                     Muscle protein; Alternative splicing; Multigene family;
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                                                                                                                                                                                                                                                                           interPro;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ALTERNATIVE PRODUCTS: AT LEAST THREE ISOFORMS ARE PRODUCED BY ALTERNATIVE SPLICING.
SIMILARITY: BELONGS TO THE TROPONIN T FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1910. Chem. 260:13699-13703(1985)
FUNCTION: TROPONIT IS THE TROPOMYOSIN-BINDING SUBUNIT OF
TROPONIN, THE THIN FILAMENT REGULATORY COMPLEX WHICH CONFERS
CALCIUM-SENSITIVITY TO STRIATED MUSCLE ACTOMYOSIN ATPASE ACTIVITY.
                                                                                                                                                                                                                                                                                        A03085; TPQJT2.
A03084; TPQJT1.
                                                                                                                                                                                                                                                                                                                         M26600;
M26599;
M11685;
M11684;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SWISS-PROT entry is copyright. It is produced through een the Swiss Institute of Bioinformatics and the E
   ERAEQORLKSO 11
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                                                                                                                                                                                                                                                        PF00992; Troponin;
                                 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Chem.
                                                                                                                                                                                                                                                                   IPR001978; Troponin.
                                                                                                     252
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                                   Conservative
                                                                                                                                      27
225
                                                                                                                                                                                                                                                                                                                         ; AAA49506.1; -.; AAA49505.1; -.; AAA49504.1; -.; AAA49503.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  264:12482-12491(1989).
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237
                                                                                                     29967
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                                   4
                                                    Score 41; |
Pred. No. 3
                                                                                                                                     MISSING (IN AN ISOFORM).
LTLRCRLQELSKF -> VTLRNRIDQAQKH
                                                                                                                                                                                  PHOSPHORYLATION (BY CK2)
                                                                                                                                                                    (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                   67FED1A595C3C997 CRC64;
                                    Mismatches
                                                                                                                                                                                                         SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
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                                                                  BB
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                                   Indels
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                                   Gaps
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                                                                  RESULT
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                                                                                                                                                                                    Query Match
Best Local S
Matches 7
TRT3_RAT s
P09739; P09740;
01-MAR-1989 (Rel
                                                    RAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TRT3_HUMAN
P45378;
                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                        Genew;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sarkar S.
                                                                                                                                                                                                                                                                                                                                                                        MIM; 600692;
                                                                                                                                                                                                                                                                                        MOD_RES
                                                                                                                                                                                                                                                                                                                                                        interPro;
                                                                                                                     101
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; M21984; AAA36777.1; -
EMBL; AF026276; AAF21629.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Isolation and characterization of human T cDNA: comparative sequence analysis of the evolution of members of a multigene f
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Troponin T, fast skeletal muscle isoform beta
                                                                                                                                                                                                                                                                                    Muscle protein; Multigene family; Phosphorylation INIT_MET 0 0 BY SINILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                               or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DNA Cell Biol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE-Fetal skeletal muscle;
MEDLINE-94226695; PubMed-8172653;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Wu Q.-L., Jha P.K.,
                                                                                                                                                                          Local Similarity
nes 7; Conserv
                                                                                                                                         1 ERAEQQRLKSQ 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ERAEQQRIRAE 108
                                                                                                             ERAEQQRIRAE 111
                                                                                                                                                                                                                                                                                                                     PF00992;
                                                                                                                                                                                                                                                                                                                                                                 HGNC:11950; TNNT3.
                                                                                                                                                                                                                                                                                                                                IPR001978; Troponin.
                                                                                                                                                                                                                                         257
(Rel. 10, Created)
                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                   Troponin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13:217-233(1994).
                                                                                                                                                                                                                                       Ą,
                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Raychowdhury
                                                                                                                                                                                       66.1%;
63.6%;
                                                                                                                                                                                                                                         30465
                                                                                                                                                                                                                                         ¥.
                                                                                                                                                                        Score 41; DB Pred. No. 4; 4; Mismatches
                                                                                                                                                                                                                                     (BY SIMILARITY). F433B3626BE597D9 CRC64;
                                                                                                                                                                                                                                                                     PHOSPHORYLATION (BY CK2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 M. K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              257
                               258
                                                                                                                                                                                                                                                                                                                                                                                                                                               (See http://www.isb-sib.ch/announce/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    n fast skeletal beta troponin
f isoforms and insight into
family.";
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                                                                                                                                                                                                         Length 257;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ToTF)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              outstation
                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-FEB-1991
15-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nadal-Ginard B.;
"Intricate combinatorial regulated troponin T isof Cell 41:67-82(1985)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Alternatively spliced exons divergence.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-86281691; PubMed-3735424;
Breitbart R.E., Nadal-Ginard B.;
"Complete nucleotide sequence of the fast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia; NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Breitbart R.E., Nguyen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. MEDLINE-85201690; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rattus norvegicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        tities requires a license agreement (S send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FUNCTION: TROPONIN T IS THE TROPOMYOSIN-BINDING SUBUNIT OF TROPONIN, THE THIN FILAMENT REGULATORY COMPLEX WHICH CONFERS CALCIUM-SENSITIVITY OF STRIATED MUSCLE ACTOMYOSIN ATPASE ACTIVITY. ALTERNATIVE PRODUCTS: AT LEAST 44 ISOFORMS ARE PRODUCED BY ALTERNATIVE SPLICING. THE ALPHA AND BETA FORMS ARE PRODUCED BY THE USE OF MUTUALLY EXCLUSIVE EXONS.

SIMILARITY: BELONGS TO THE TROPONIN T FAMILY.
M15202 AAA964411

M15202 AAA9664611

M15202 AAA9665311

M15202 AAA9666311

M15202 AAA9666311

M15202 AAA9666711

M15202 AAA9664711

M15202 AAA9664711

M15202 AAA9664711

M15202 AAA9664711

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          188:313-324(1986).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17,
41,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PubMed-2986851;
guyen H.T., Medford
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (Rat).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       patterns of forms from a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     muscle
      ce of the fast skeletal troponin exhibit unusual interspecies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Craniata; Vertebrata; I
Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 isoforms beta/alpha
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   exon splicing single gene.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Euteleostomi;
; Murinae; Rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (Beta/alpha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mahdavi
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Best Local S
Matches
                                                                                                                                                                         SEQUENCE FROM N.A.

MEDLINE-89066672; PubMed-3198600;

MEDLINE-89066672; PubMed-3198600;

Smillie L.B., Golosinska K., Reinach F.C.;

Smillie L.B., Golosinska K., Reinach F.C.;

Smillie L.B., Golosinska K., Reinach F.C.;

Sequences of complete cDNAs encoding four variants of chicken skeletal muscle troponin T.";

J. Biol. Chem. 263:18816-18820(1988).

-i- FUNCTION: TROPONIN T IS THE TROPOMYOSIN-BINDING SUBUNIT OF TROPONIN, THE THIN FILAMENT REGULATORY COMPLEX WHICH CONFERS CALCIUM-SENSITIVITY TO STRIATED MUSCLE ACTOMYOSIN ATPASE ACTIVITY.

-i- ALTERNATIVE BRODUCTS: AT LEAST 4 ISOFORMS; TMT-1, TWT-2, TMT-3, SIGWN HERE) AND TMT-4; ARE PRODUCED BY ALTERNATIVE SPLICING.

-i- SIMILARITY: BELONGS TO THE TROPONIN T FAMILY.
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                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TRT3_CHICK STANDARD; PRT; 262 AA.
P12620; P12621; P12619; P12618;
01-OCT-1989 (Rel. 12, Created)
01-FEB-1991 (Rel. 17, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Troponin T, fast skeletal muscle isoforms.
Gallus Gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Archosauria; Aves; Neognathae; Galliformes; Phasiani
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INIT_MET 0
MOD_RES 1
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M15202; AAA96465.1; -...
L; M15202; AAA96470.1; -...
L; M15202; AAA96470.1; -...
L; M15202; AAA96471.1; -...
L; M15202; AAA96472.1; -...
L; M15202; AAA96477.1; -...
L; M15202; AAA96477.1; -...
L; M15202; AAA96477.1; -...
L; M15202; AAA96470.1; -...
L; M1
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(BY SIMILARITY).
MISSING (IN SOME CLASS I ISOFORMS
MISSING (IN SOME CLASS I ISOFORMS).
MISSING (IN CLASS II ISOFORMS).
MISSING (IN CLASS II ISOFORMS).
MISSING (IN CLASS III ISOFORMS).
MISSING (IN CLASS III ISOFORMS).
MISSING (IN CLASS III ISOFORMS).
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37BDD772A4F28C7E CRC64;
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NG (IN SOME CLASS I ISOFORMS).
NG (IN CLASS II ISOFORMS).
NG (IN CLASS II ISOFORMS).
NG (IN CLASS IV ISOFORMS).
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                    http://www.isb-sib.ch/announce/
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EMBL; M22158; AAA49101.1; -
EMBL; M22155; AAA49101.1; -
EMBL; M22154; AAA49100.1; -
PIR; A31957; A31957,
PIR; A31957; B31957,
PIR; C31957; B31957,
PIR; C31957; B31957;
PIR; D31957; D31957;
PIR; D31957; D31957;
PIR; D31957; D31957;
PIR; D31957; D31957
          STRAIN-New Zealand white; TISSUE-Skeletal muscle;
MEDIZINE-90323375; pubwed-2373251;
Briggs M.M., McGinnis H.D., Schachat F.;
"Transitions from fetal to fast troponin T isoforms are coordinated with changes in tropomyosin and alpha-actinin isoforms in developing rabbit skeletal muscle.";
                                                                                                                Briggs M.M., Schachat F.;
"Origin of fetal troponin T: developmentally new exon in the fast troponin T gene.";
Dev. Biol. 158:503-509(1993).
                                                                                                                                                                                                                                             Pearlstone J.R., Johnson P., Carpenter M.R., "Primary structure of rabbit skeletal muscle determination of the NH2-terminal fragment CE sequence of troponin-T.", Biol. Chem. 252:983-989(1977).
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21-JUL-1986 (Rel. 01, Created)
01-OCT-1996 (Rel. 34, Last sequence update;
15-JUN-2002 (Rel. 41, Last annotation update;
Troponin T, fast skeletal muscle isoforms.
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SEQUENCE OF 1-66 FROM N.A., AND ALTERNATIVE SPLICING.
STRAIN-New Zealand white; TISSUE-Skeletal muscle;
MEDLINE-93345743; PubMed-8344466;
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MEDLINE=77118575; PubMed=320204;
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Mammalia; Eutheria;
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7; Conserv
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Metazoa; Chordata; C:
utheria; Lagomorpha;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              262 AA;
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MISSING
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Pred. No.
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EEYEEEAHBAEEVHEEEVHEPAPP -> AHEAEEVHEEAHH
EEAHHAEAHHEEAHAHAEEVHE (IN ISOFORM TNT-
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DOAOKH -> LTLRCRLQELSKF
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troponin-T. S
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EMBL; U04970; AAA16023.1; -.
EMBL; U04971; AAA16025.1; -.
EMBL; U04973; AAA16026.1; -.
EMBL; U04973; AAA16027.1; -.
EMBL; U04974; AAA16028.1; -.
EMBL; U04975; AAA16028.1; -.
EMBL; U04975; AAA16029.1; -.
EMBL; U04976; AAA16030.1; -.
EMBL; U04976; AAA16031.1; -.
EMBL; U04978; SAAA16031.1; -.
EMBL; U04978; AAA16031.1; -.
EMBL; U04978; AAA16030.1; -.
EMBL; 
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MEDLINE-7157104; PubMed-849266;
Moir A.J.G., Cole H.A., Perry S.V.;
Moir A.J.G., Cole H.A., Perry S.V.;
Moir A.J.G., Cole H.A., Perry S.V.;

"The phosphorylation sites of troponin T from white skeletal muscle and the effects of interaction with troponin C on their phosphorylation by phosphorylase kinase.";
Blochem, J. 161:371-382(1977).

"I FUNCTION: TROPONIN T IS THE TROPOMYOSIN-BINDING SUBUNIT OF TROPONIN, THE THIN FILAMENT RESULATORY COMPLEX WHICH CONFERS CALCIUM-SENSITIVITY TO STRIATED MUSCLE ACTOMYOSIN ATPASE ACTIVITY.

"I-ALTERNATIVE PRODUCTS: 9 ISOFORMS; TWT1 (SHOWN HERE), TWT1F, TWT2.

"INTERNATIVE SPLICING.
ALTERNATIVE SPLICING.
ALTERNATIVE SPLICING.
ALTERNATIVE SPLICING.
ALTERNATIVE SPLICING.
ALTERNATIVE SPLICING.

"TO SER-168 OR SER-169 AND SER-175 OR SER-176 ARE PHOSPHORYLATED TO STRIATED TO STRIATE
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Briggs M.M., Schacnac F.,
"N-terminal amino acid sequences
"N-terminal amino acid sequences
troponin T isoforms from rabbit f
r Mol. Biol. 206:245-249(1989).
CONFLICT
CONFLICT
CONFLICT
SEQUENCE
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MOD_RES
MOD_RES
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STRAIN=New Zealand white; TISSUE-Skeletal muscle;
MEDLINE-89199646; PubMed-2704041;
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Briggs M.M., Schachat F.;
Submitted (JAN-1994) to the
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19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   family; Phosphorylation;
                                                               PHOSPHORYLATION (BY CK2).
MISSING (IN ISOFORM TNT4F).
TNT2.5F AND ISOFORM TNT3, II
AND ISOFORM TNT4F).
MISSING (IN ISOFORM TNT2, II
AND ISOFORM TNT2, II
AND ISOFORM TNT2, II
AND ISOFORM TNT2, II
OFFORM TNT2, II
OFFORM TNT4F).
MISSING (IN ISOFORM TNT1F, II
OFFORM TNT2FA, ISOFORM TNT1F, II
OFFORM TNT2FA, ISOFORM TNT4F).
UN -> E (IN REF, 1).
UN -> H (IN REF, 1 AND 5).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ACETYLATION
       3D5A7E5F661E4CA9
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                             E (IN SEF. 1 A)
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                                            . 1).
EF. 1 AND 5).
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       CRC64;
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                                                                                                                                                                                                                                                                                                ISOFORM THT2FA
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                                                                                                                                                                                                                                                                                                                                                                                                                                       ISOFORM
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                                                                                                                                                                                       ISOFORM
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RESULT 9
TRT2_SHEEP
ID TRT2_S
AC P50751
DT 01-OCT
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TRT2_BO
                                                                                                                                                                  Query Match
Best Local S
Matches 7
  TRT2_SHEEP
P50751;
01-OCT-1996
01-OCT-1996
                                                                                                                                                                                                                                 MOD_RES
MOD_RES
WOD_RES
VARSPLIC
                                                                                                                                                                                                                                                                                                                                                      Noland T.A. JI., Raynor R.L., Kuo J.F.;

"Identification of sites phosphorylated in bovine cardiac troponin I and troponin T by protein kinase C and comparative substrate activity of synthetic peptides containing the phosphorylation sites.";

-I. Biol. Chem. 264:20778-20785(1989).

-I. FUNCTION: TROPONIN T IS THE TROPOMYOSIN-BINDING SUBBUIT OF TROPONIN, THE THIN FILAMENT REGULATORY COMPLEX WHICH CONFERS CALCIUM-SENSITIVITY TO STRIATED MUSCLE ACTOMYOSIN ATPASE ACTIVITY.

-I. ALTERNATIVE PRODUCTS: 2 isoforms; 1 (shown here) and 2; are produced by alternative splicing.

-I. SIMILARITY: BELONGS TO THE TROPONIN T FAMILY.

PIR; A28008; A28008.
                                                                                                                                                                                                                                                                                                                              Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  P13789; P13790;
01-JAN-1990 (Rel. 13, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Troponin T, Cardiac muscle isoforms (TnTC).
                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Ch
Mammalia; Eutheria; Ce
Bovidae; Bovinae; Bos.
NCBI_TaxID=9913;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-88107637; PubMed-3122824;
Leszyk J., Dumaswala R., Potter J.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bos taurus (Bovine).
Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BOVIN
                                                                                                                                                                                                                                                                                                      MOD_RES
                                                                                                                                                                                                                                                                                                                    Muscle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-90062225; PubMed-2584239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Biochemistry 26:7035-7042(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tobacman L.S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                              InterPro; IPR001978; Troponin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PHOSPHORYLATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Bovine cardiac troponin T: amino isoforms.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TRT2_BOVIN
                                                                                                             130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           122
                                                                                                                                       1 ERAEQQRLKSQ
                                                                                                             ERAEQQRIRAE 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ERAEQQRLKSQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ERAEQQRIRAE 132
                                                                                                                                                                                                                                                                                                protein; Alternative splicing; Phosphorylation.
1 1 PHOSPHORYLATION (BY CK2)
                                                                                                                                                                  7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity 63.
                                                                                                                                                                                                                      190
199
280
16
284 AA;
  (Rel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     aswala R., Pot
Collins J.H.;
                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
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34, Created)
34, Last sequence update)
                                                                                                                                                                                                                                    190
199
280
21
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                                                                                                                                                                                                                       33782 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cetartiodactyla;
                                                                                                                                                                              66.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            66.1%;
                                                                                                                                                                  4
                                                                                                                                                                           Score 41;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score
Pred.
                                                                                                                                                                                                                    PHOSPHORYLATION (B)
AAEEEH -> N (IN ISC)
087F3A59A5138530
                                                                                                                                                                                                                                                            (BY SIMILARITY). PHOSPHORYLATION PHOSPHORYLATION
                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ed. No. 4.3;
Mismatches
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                                          286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gusev N.B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4.3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sequences
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                                                                                                                                                                                           Length 284;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        of the two
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Verin A.D.,
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TRT2_HUMAN
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Best Local S
Matches 7
                                                                                                                                                                                                                                                                                                                                                                   TRT2_HUMAN STANDARD; PRT; 2
P45379; Q99596; Q99597; O60214;
01-NOV-1995 (Rel. 32, Created)
15-JUN-2002 (Rel. 41, Last sequence up
15-JUN-2002 (Rel. 41, Last annotation
Tropponin T, cardiac muscle isoforms (T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pediatr Res. 29:580-585(1991).

1. FUNCTION: TROPONIN T IS THE TROPOMYOSIN-BINDING SUBUNIT OF TROPONIN, THE THIN FILAMENT REGULATORY COMPLEX WHICH CONFERS CALCIUM-SENSITIVITY TO STRIATED MUSCLE ACTOMYOSIN ATPASE ACTIVI-1. DEVELOPMENTAL STAGE: EXPRESSED FROM MIDGESTATION TO ADULT LIFE.

1. SIMILARITY: BELONGS TO THE TROPONIN T FAMILY.

InterPro; IPR001978; Troponin; 1.

Prom; PF00992; Troponin; 1.
TISSUE-Fetal heart;
MEDLINE-96129582; F
                                                                                           Townsend P.J., Farza H., Macgeoch C.,
Gahlman R., Yacoub M.H., Barton P.J.R.
                                                                                                                                       TISSUE-Heart
                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Muscle protein; Multigene family; Phosphorylation INIT_MET 0 BY SIMILARITY. MOD_RES 1 1 PHOSPHORYLATION (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE=Fetal heart;
MEDLINE=91326551; PubMed-1866215;
MCAULIffe J.J., Robbins J.;
"Troponin T expression in normal and pressure-loaded
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mammalia; Eutheria;
Bovidae; Caprinae; (
NCBI_TaxID=9940;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15-JUN-2002 (Rel. 41, Last annotation update) Troponin T, cardiac muscle isoform (TnTC).
                            SEQUENCE FROM N.A.
                                                                  "Human cardiac tro
                                                                                                                       TISSUE-Heart muscle;
MEDLINE-94375053; PubMed-8088824;
                                                                                                                                                                                                                                 Mesnard L., Samson
                                                                                                                                                                                                                                               MEDLINE-93345675; PubMed-8344420;
                                                                                                                                                                                                                                                               TISSUE-Heart;
                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                  NCBI_TaxID-9606;
                                                                                                                                                                                                                                                                                                                                           Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ovis aries
                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                              "Molecular cloning
troponin T.";
                                                                                                                                                                                                                    Mercadier J.-J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ERAEQORLKSO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity 63. 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (Sheep).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    286
                                                                troponin T: identification of fetal the TNNT2 locus to chromosome 1q.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AA;
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                                                                                                                                                  (ISOFORMS 1 AND
                          (SPLICED
                                                                                                                                                                                                                                                                       (ISOFORM
                                                                                                                                                                                                                                                                                                                Chordata;
Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    33633 MW;
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                                                                                                                                                                                                        developmental
                                                                                                                                                                                                                                 Espinasse
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 41; DB
Pred. No. 4.4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (BY SIMILARITY)
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                                                                                                                                                                                                                                                                                                                Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    E59A00F8B3731B11 CRC64;
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developing
J. Mol. Cel
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Circ.
                                                                                              MEDLINE-95206332; PubMed-7898523;
Watkins H., McKenna W.J., Thierfelder L.,
O'Donoghue A., Spirito P., Matsumori A.,
                                                                                                                                                         Thierfelder L., Watkins H., Macrae C., Lamas R., Vosberg H.-P., Seidman J.G., Seidman C.E.;
"Alpha-tropomyosin and cardiac troponin T mutatic hypertrophic cardiomyopathy: a disease of the sar Cell 77:701-712(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM
D'Cruz L.G.. (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Anderson P.A., Creig A., Mark T.M., Malouf Ungerleider R.M., Allen P., Kay B.K.; "Molecular basis of human cardiac troponin the developing, adult, and failing heart."; Circ. Res. 76:681-686(1995).
                                                                                                                                                                                                                                                          "The major protein expression profile and database of human heart."; Electrophoresis 16:1160-1169(1995).
                                                                                                                                                                                                                                                                                                                                                                      Farza H., Townsend P.J.;
Submitted (FEB-1997) to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "A rapid protocol for cardiac troponin 'A rapid protocol for cardiac troponin familial hypertrophic cardiomyopathy."; Hum. Mutat. 11:179-182(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-95202803; PubMed-7534662; Anderson P.A., Greig A., Mark T.M
VARIANT FHC PRO-287.
Erdmann J., Wischke S., Kallisch
Fleck E., Regitz-Zagrosek V.;
                                            "Mutations in the genes for cardiac E
in hypertrophic cardiomyopathy.";
New Engl. J. Med. 332:1058-1064(1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (JUN-2001) to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=95202804; PubMed=7895342; Mesnard L., Logeart D., Taviaux S
                                                                                                                                       VARIANTS FHC
                                                                                                                                                                                                                       MEDLINE-94265260;
                                                                                                                                                                                                                                    VARIANTS FHC ASN-88 AND
                                                                                                                                                                                                                                                                                                Ershova E.S., Egorov T.A.,
                                                                                                                                                                                                                                                                                                         Kovalyov L.I.,
                                                                                                                                                                                                                                                                                                          MEDLINE-96007936; PubMed-7498159;
Kovalyov L.I., Shishkin S.S., Efimochkin A.S.,
                                                                                                                                                                                                                                                                                                                                       TISSUE-Heart
                                                                                                                                                                                                                                                                                                                                                 SEQUENCE OF
                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE-Blood
                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE OF 190-228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-98141687; PubMed-9482583;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE-Heart muscle;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. (ISOFORM 6),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            the normal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Human cardiac troponin T: cloning
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. (ISOFORMS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. (ISOFORMS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Townsend
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Molecular cloning
                                                                                      C.E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ing and failing heart.";
Cell. Cardiol. 27:2223-2236(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 76:687-692(1995).
                                                                                                                                                                                                                                                                                                                                                 69 - 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N.A. (ISOFORM 6).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           failing heart.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Barton P.J.R., Yacoub M.H., Farza H.; ing of human cardiac troponin T isoforms:
                                                                                                                                                                                                                                                                                                                                               AND
                                                                                                                                                                                                                         PubMed-8205619;
                                                                                                                                                                                                                                                                                                                                                                                                             AND
                                                                                                                                                                                                                                                                                                                                               176-181
                                                                                                                                                                                                                                     GLN-101
                                                                                                                                                                                                                                                                                                                                                                                                             230-287
                                                                                                                                                                                                                                                                                                                                                                                                                                    the EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                        the EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                Musalyamov
                                                                        cardiac troponin
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Moravec C.
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S., Seidman J.G.,
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detection
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use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                           here), 2, 3, 4, 5, 6/TNT3, 7/TNT4, 8/TNT2, 9 and 10; may be produced by alternative splicing.

-: TISSUE SPECIFICITY: Heart. The fetal heart shows a greater expression in the atrium than in the ventricle, while the adult heart shows a greater expression in the ventricle than in the atrium. Isoform 6 predominates in normal adult heart. Isoforms 1, 7 and 8 are expressed in fetal heart. Isoform 7 is also expressed in falling adult heart.

-! DISEASE: DEFECTS IN TNNT2 ARE ONE OF THE CAUSES OF FAMILIAL HYPERTROPHIC CARDIOMYOPATHY (FHC) WHICH IS AN AUTOSOMAL DOMINANT DISORDER CHARACTERIZED BY INCREASED MYOCARDIAL MASS WITH MYOCYTE AND MYOFIBRILLAR DISARRAY. THIS FORM OF FHC IS KNOWN AS CMH2.

IT IS A DISEASE OF THE SARCOMERE.

-!- SIMILARITY: BELONGS TO THE TROPONIN T FAMILY.
                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics institute. There are no restrictions on its the European Bioinformatics institute. There are no restrictions on its the European Bioinformatics institute. There are no restrictions on its the European Bioinformatics institutions as long as its content is in no way use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "A new mutation of the cardiac troponin ? hypertrophic cardiomyopathy without left
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hum. Mutat.
EMBL;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FUNCTION: TROPONIN T IS THE TROPOMYOSIN-BLINDING CONFERS TROPONIN, THE THIN FILAMENT REGULATORY COMPLEX WHICH CONFERS CALCIUM-SENSITIVITY TO STRIATED MUSCLE ACTOMYOSIN ATPASE ACTIVITY. ALTERNATIVE PRODUCTS: At least 10 isoforms; isoform 1/TNT1 (shown harman 2. 3, 4, 5, 6/TNT3, 7/TNT4, 8/TNT2, 9 and 10; may be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                novel missense Arg 278 Pro mutation in the troponin T gene
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ALT_SEQ.
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EMBL; InterPro, IPR001978; Troponin.

InterPro, IPR001978; Troponin; 1.

Pfam; PF00992; Troponin; 1.

Muscle protein; Alternative splicing; Multigene f
Muscle protein; Nispase mutation; Polymorphism; EMBL; EMBL; Genew; S64668; AAB27731.1; A
X74819; CAA52818.1;
L440162; AAA67422.1;
X79856; CAA56235.1;
X79856; CAA56237.1;
X79857; CAA56237.1;
X79858; CAA56238.1;
X79858; CAA70840.1;
Y09627; CAA70841.1;
Y09628; CAA70841.1; ; AY044273; AAK92231 ; S71128; AAB30957.1 ; S71127; AAB30957.1 w; HGNC:11949; TNNT; AF004410; AAC39590.1 AF004411; AAC39590.1 AF004413; AAC39590.1 AF004414; AAC39590.1 AF004414; AAC39590.1 AF004415; AAC39590.1 AF004416; AAC39590.1 AF004417; AAC39590.1 AF004418; AAC39590.1 AF004418; AAC39590.1 AF004418; AAC39590.1 AF004421; AAC39590.1 AF004421; AAC39590.1 AF004422; AF004409; Disease mutation; JOINED
JOINED Cardiomyopathy

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P SEQUENCE FROM N.A.

P SEQUENCE FROM N.A.

REDILINE-93059379; PubMed-1433301;

XA Jin J.-P., Huang Q.Q., Yeh H.I., Lin J.J.C.;

RT "Complete nucleotide sequence and structural organization of rat recardiac troponin T gene. A single gene generates embryonic and adult reduction via developmentally regulated alternative splicing.";

RT 150forms via developmentally regulated alternative splicing.";

RL J. Mol. Biol. 227:1269-1276(1992).

CC 1FONOTION: TROPONIN T IS THE TROPOMYOSIN-BINDING SUBUNIT OF TROPONIN, THE THIN FILAMENT REGULATORY COMPLEX WHICH CONFERS CC CALCIUM-SENSITIVITY TO STRIATED MUSCLE ACTOMYOSIN ATPASE ACTIVITY.

CC 1- ALTERNATIVE PRODUCTS: 2 isoforms; 1/smbryonic form (shown here)

CC and 2/Adult form; are produced by alternative splicing.

CC -1- SIMILARITY: BELONGS TO THE TROPONIN T FAMILY.

CC -1- SIMILARITY: BELONGS TO THE TROPONIN T FAMILY.
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                                                                                                                                                                                                                                              Jin J.-P., Lin J.C.; "Isolation and characterization of cDNA clones adult isoforms of rat cardiac troponin T."; J. Biol. Chem. 264:14471-14477(1989).
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                                                                                                                                                                                                                                                                                         MEDLINE-89340569; Pu
Jin J.-P., Lin J.C.;
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Mammalia; Eutheria;
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                                s SWISS-PROT entry is copyright. It is produced through ween the Swiss Institute of Bioinformatics and the Extenopean Bioinformatics Institute. There are no restriby non-profit institutions as long as its content
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7; Conserv
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Rodentia;
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Pred. No.
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MISSING (IN FHC CMH2)
/FTId-VAR_007608.
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F -> I (IN FHC CMH2).
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R -> L (IN FHC CMH2).
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1 9).
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                                                              VARSPLIC
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SEQUENCE
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01-OCT-1996
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Mus musculus (Mouse).
Mus musculus (Mouse).
Metazoa; Chordata; Metazoa; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VARSPLIC CONFLICT
                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bloinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Jin J.-P., Wang J., Zhang J.;
Submitted (JAN-1996) to the EmbL/GenBank/DDBJ databases.

1- FUNCTION: TROPONIN T IS THE TROPOMYOSIN-BINDING SUBUNIT OF
TROPONIN, THE THIN FILAMENT REGULATORY COMPLEX WHICH CONFERS
CALCIUM-SENSITIVITY TO STRIATED MUSCLE ACTOMYOSIN ATPASE ACTIVITY.

1- ALTERNATIVE PRODUCTS: 2 ISOFORMS, EMBRYONIC/EA (SHOWN HERE) AND
A3B; ARE PRODUCED BY ALTERNATIVE SPLICING.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL;
                                                                                                                                                   Phosphorylation.
INIT_MET 0
MOD_RES 1
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EMBL; L47600; AAA85352.1;
MGD; MGI:104597; Tnnt2.
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INIT_MET 0
MOD_RES 1
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Pfam; PF00992; Troponin; 1.
Muscle protein; Alternative splicing; Multigene family;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           - 1 - SIMILARITY: BELONGS TO THE TROPONIN T FAMILY.
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                                                                                                                                                                                                                                                          nterPro; IPR001978; Troponin.
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                                                                                                                                                                                                                                    PF00992; Troponin;
                                                                                                                                                                                                                  protein; Alternative splicing; Multigene
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Pred. No.
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T -> A (IN REF. 2).
; 60EB44A8E9DF5E27 CRC64;
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                    Length 300;
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P09495;
01-MAR-1989
01-MAR-1989
15-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                        *Structure and complete nucleotide sequence of the gene encoding rat fibroblast tropomyosin 4, ", J. Mol. Biol. 213:399-405(1990).

7. Mol. Biol. 213:399-405(1990).

7. Hol. Biol. 213:399-405(1990).

8. FUNCTION: Binds to actin filaments in muscle and nonmuscle cells. Plays a central role, in association with the troponin complex, in the calcium dependent regulation of vortebrate striated muscle contraction. Smooth muscle contraction is regulated by interaction with caldesmon. In nonmuscle cells is implicated in stabilizing cytoskeleton actin filaments.

9. SUBUNIT: DIMER OF AN ALPHA AND A BETA CHAIN.

10. DOMAIN: THE MOLECULE IS IN A COILED COIL STRUCTURE. THE SEQUENCE EXHIBITS A PROMINENT SEVEN-RESIDUES PERIODICITY.

11. SIMILARITY: BELONGS TO THE TROPOMYOSIN FAMILY.
                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation—the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE-Liver, and Brain;
MEDLINE-90278950; PubMed-2112608;
Lees-Miller J.P., Yan A., Helfman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "zamawaki-Kataoka Y., Helfman D.M.;
"Isolation and characterization of cDNA clones encoding a molecular weight nonmuscle tropomyosin isoform.";
J. Biol. Chem. 262:10791-10800(1987).
                                                                                                                                                                 Pfam; PF00261; Tropomyosin; 1. PRINTS; PR00194; TROPOMYOSIN. PROSITE; PS00326; TROPOMYOSIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                    Muscle protein; Cytoskeleton; Multigene family.
                                                                                                                                                                                                                              PIR; A28493; A28493
PIR; S10623; S10623
                                                                                                                                                                                                                                                           EMBL; J02780; AAA42291.1; EMBL; Y00169; CAA68360.1;
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 145
                                                            Local Similarity
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                                                                                                                                                                                                              IPR000533; Tropomyosin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (Rel. 10, Created)
(Rel. 10, Last sequence up
(Rel. 41, Last annotation
alpha 4 chain (Tropomyosin
                                                                                                                        248
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4 chain (Tropomyosin 4) (TM-4).
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Rodentia;
                                                                                                                      28509 MW;
                                                                          64.58;
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                                                                        Score 40; I
Pred. No. 5.
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                                                                                                                                                  Actin-binding; Coiled coil;
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                                                                                                                      53C9327CA60CF954 CRC64;
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                                                                          DB 1;
5.7;
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RESULT 14
GRPE_STRPY
IDD _GRPEPY
AC 0997C
OT 16-00
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GRPE GRPEPY
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099YC8; P82581;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2002 (Rel. 40, Last sequence up
15-JUN-2002 (Rel. 41, Last annotation
GrpE protein (HSP-70 cofactor).
GRPE OR SPY1761 OR SPYM18_1832.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN-MGAS8232 / Serotype M18;
MEDLINE-21927593; PubMed-11917108;
Smoot J.C., Barbian K.D., Van Gompel J.J., Smoot L.M., Chaussee M.S.,
Sylva G.L., Sturdevant D.E., Ricklefs S.M., Porcella S.F.,
Parkins L.D., Beres S.B., Campbell D.S., Smith T.M., Zhang Q.,
Kapur V., Daly J.A., Veasy L.G., Musser J.M.;
"Genome sequence and comparative microarray analysis of serotype M18
group A Streptococcus strains associated with acute rheumatic fever
                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ferretti J.J., McShan W.M., Ajdic D.J., Savic D.J., Savic G., Lyon K., Primeaux C., Sezate S., Suvorov A.N., Kenton S., Lai H.S., Lin S.P., Qian Y., Jia H.G., Najar F.Z., Ren Q., Zhu H., Song L., White J., Yuan X., Clifton S.W., Roe B.A., McLaughlin R.; "Complete genome sequence of an Ml strain of Streptococcus pyogenes."; "Proc. Natl. Acad. Sci. U.S.A. 98:4658-4663(2001).
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                                                                                                                                                                            InterPro; IPR000740; GrpE.
pfam; PF01025; GrpE; 1.
PRINTS; PR00773; GRPEPROTEIN.
PROSITE; PS01071; GRPE; 1.
Chaperone; Heat shock; Complete
                                                                                                                                                                                                                                                                                                                               EMBL; AE006604; AAK34502.1; -. EMBL; AE010089; AAL98350.1; -. HSSP; P09372; 1DKG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. STRAIN-MGAS8232 /
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         proteins."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Two-dimensional gel electrophoresis map of Streptococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VanBogelen R.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hogan D.A., Du P., Stevenson T.I., Whitton M., Kilby G.W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PARTIAL SEQUENCE, AND MASS SPECTROMETRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=1314, 186103;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        mitted (MAY-2000) to the SWISS-PROT data bank. FUNCTION: STIMULATES, JOINTLY WITH DNAJ, THE ATPASE ACTIVITY OF DNAK. HELPS TO RELEASE ADP FROM DNAK THUS ALLOWING DNAK TO RECY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MORE EFFICIENTLY (BY SIMILARITY).

MASS SPECTROMETRY: MW-22054.54; METHOD-Electrospray.
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                                                                                                                                                   22054 MW;
                                                        62.9%;
                         Score 39; DB 1;
Pred. No. 6.4;
2; Mismatches
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RESULT 15
TRT1_HUMAN
IDT TRT1_H
AC P13805
DT 01-NOV
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DE Tropon
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RN (1]
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RT domair
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RA ROSES
RT From 2
RI Genom
CC -1- FI
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RR SEQUE
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                                                                                                EMBL; M19309; AAA61204.1; -. EMBL; M19308; AAA61205.1; -. EMBL; S69208; AAB30272.1; -. EMBL; S69209; AAB30273.1; -. EMBL; AJ011712; CAA09751.1; -. EMBL; AJ011713; CAA09751.1; JO EMBL; AJ011712; CAA09752.1; -. EMBL; AJ011713; CAA09752.1; JO EMBL; AJ011713; CAA09752.1; JO PIR; A29783; A29783.
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01-NOV-1995 (Rel. 32, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Troponin T, slow skeletal muscle isoforms (Slow troponin T).
TNNT1 OR TNT.
Homo san' (---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
MEDLINE-88058976; PubMed-2824479;
Gahlmann R., Troutt A.B., Wade R.P., Gunning P., Kedes L.;
Gahlmann R. Troutt A.B., Waternation important functional alternative splicing generates variants in important functional domains of human slow skeletal troponin T.*;
T niol. Chem. 262:16122-18126(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.

MEDLINE-99208666; PubMed-10191089;

Barton P.J.R., Cullen M.E., Townsend P.J., Brand N.J., Mullen A.J.,

Norman D.A.M., Bhavsar P.K., Yacoub M.H.;

"Close physical linkage of human troponin genes; organization,

sequence, and expression of the locus encoding cardiac troponin I and
slow skeletal troponin T.";

Genomics 57:102-109(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalla; Eutheria; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Samson F., Mesnard L., Mihovilovic M., Potter T.G., Mercadier J.*. Roses A.D., Gilbert J.R., Roses A.D., Gilbert J.R., "A new human slow skeletal troponin T (TnTs) mRNA isoform derived from alternative splicing of a single gene."; Blochem. Blophys. Res. Commun. 199:841-847(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
TISSUE-Skeletal muscle;
MEDLINE-94183266; PubMed-8135831;
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                                         nterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FUNCTION: TROPONIN T IS THE TROPOMYOSIN-BINDING SUBUNIT OF TROPONIN, THE THIN FILAMENT REGULATORY COMPLEX WHICH CONFERS CALCIUM-SENSITIVITY TO STRIATED MUSCLE ACTOMYOSIN ATPASE ACTIVITY. ALTERNATIVE PRODUCTS: 3 ISOFORMS; 1 (SHOWN HERE), 2 AND 3; ARE PRODUCED BY ALTERNATIVE SPLICING.
SYMILARITY: BELONGS TO THE TROPONIN T FAMILY.
                                     IPR001978; Troponin.
   Troponin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
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VARSPLIC
CONFLICT
SEQUENCE
                                                                                                                    Muscle protein; Phosphorylation; Alternative splicing; Multigene family.

INIT_MET 0 0 PHOSPHORYLATION (BY CK2)

MOD_RES 1 1 PHOSPHORYLATION (BY CK2)
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MISSING (IN ISOFORM 2).
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                                              Score 39;
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Search completed: March 13, 2003, 18:49:55 Job time: 7.85455 secs

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Run
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AAP90120
                                                                                                                                                                                                                                                                                 SUMMARIES
                                                                        Human soluble CD23
Human soluble CD23
Sequence containin
IgE binding factor
Recombinant Fc_eps
Low affinity Fc_ep
                  Fc gamma receptor.
Human IgE binding
Sequence encoded b
                                                                                                                                                                                                                     Description
Human lymphocyte
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S. pneumoniae grpE	AAY11233	18	139	59.7	37	5
Canine ribosome re	AAW89721	20		61.3	38	4
Amino acid sequenc	AAG67538	22	1240	61.3	38	ü
Human protein SEQ	AAM79523	22	1003	61.3	38	2
Human protein SEQ	AAM78539	22	977	1.	38	Ξ
Amino acid sequenc	AAW59881	19	977		38	ö
colo	AAB53448	21	909	1.	38	39
Amino acid sequenc	AAG67537	22	488	1.	38	8
acti	ABB91761	23	460	61.3	38	37
Pinus radiata cell	AAB25468	21	235	۲.	38	8
	ABB64076	22	2122	2	39	ŭ
Drosophila melanog	ABB70189	22	2042	ν.	39	4
	AAU19565	22	517	۲.	39	ü
	ABP28849	23	190	'n	39	2
tococcu	ABP28848	23	190	٢	39	<u> </u>
	AAU16174	22	146	62.9	39	ŏ
	AAG01801	21	131	'n	39	9
	ABP01391	23	99	Ν	39	8
Ħ	AAY91088	21	288	66.1	41	27
Human troponin T c	AAB12186	21	288	•	41	9
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cardiac	AAW4 1574	19	288	66.1	41	24
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cytoskel	AAY91961	21	269	•	41	6
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fast		21	258		41	L 7
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IgE	AAP83022	9	300	5	53	5
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ALIGNMENTS

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RESULT 1
AAW13146
PTT DDRX PAX PTT
                                          (LYNC/) LYNCH R G.
(MATS/) MATSUI M.
(NUNE/) NUNEZ R M.
(YODO/) YODOI J.
                                                                                                                                                                                                                          AAW13146 standard; Protein; 166 AA
                     N-PSDB;
                      WPI; 1997-159094/15.
N-PSDB; AAT61959.
                                                                                28-DEC-1994;
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                                                                                                              04-FEB-1997.
                                                                                                                             JP09028385-A
                                                                                                                                           Homo sapiens
                                                                                                                                                         Human; soluble; CD23; complementarity determining; isoform D; recombinant production.
                                                                                                                                                                                Human soluble CD23 isoform
                                                                                                                                                                                               17-JUN-1997
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DNA sequence encoding a soluble isoform of CD23 - scale preparation of the protein

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RESULT 2
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ID AAW1
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(MATS/) MATSUI M.
(NUNE/) NUNEZ R M.
(YODO/) YODOI J.
                                                                                                                                                                                                                                                                                        The cDNA encoding the present sequence, human soluble CD23 isoform C, can be used for the large scale recombinant proof soluble CD23.
                                                                                                                                                                                          The specification states that the nucleotide sequences contained in figures 4a-b, 5a-b, 12a-12b and 13a-b are claimed, however this numbering scheme does not relate to the scheme used in the relevant sections of the specification.
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                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; Figure 15; 33pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                     DNA sequence encoding a soluble isoform scale preparation of the protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1997-159094/15.
N-PSDB; AAT61961.
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                                                                      91.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       91.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ć.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Japanese.
                                                  0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 57;
Pred. No.
                                               Score 57; DB 18;
Pred. No. 0.053;
); Mismatches 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 18;
0.053;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 of CD23
                                                  0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ı
                                                                                          Length 167;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                              useful for large
                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 166
                                                                                                                                                                                                                                                                                                              production
                                               0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0,
                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                               0
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RESULT 4
AAP70105
ID AAP7
XX
AC AAP7
AC AAP7
DT 04-F
XX
DT 04-F
XX
XX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 3
AAW13143
ID AAW1
XX
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             밁
                                                                                                                                                                   Query Match
Best Local :
                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                            (LYNC/) LYNCH R G.
(MATS/) MATSUI M.
(NUNE/) NUNEZ R M.
(YODO/) YODOI J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Key
Peptide
                                                                                                                                                                                                                The CDNA encoding the present sequence, which contains human soluble CD23 isoform B, can be used for the large scale recombinant production of soluble CD23.

The specification states that the nucleotide sequences contained in figures 4a-b, 5a-b, 12a-12b and 13a-b are claimed, however this numbering scheme does not relate to the scheme used in the relevant sections of the specification.
                                                 AAP70105;
                                                                  AAP70105 standard;
                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                               Claim 1; Pages 18-20; 33pp; Japanese.
                                                                                                                                                                                                                                                                                                                   DNA sequence encoding a soluble isoform scale preparation of the protein
                                                                                                                                                                                                                                                                                                                                              WPI; 1997-159094/15.
N-PSDB; AAT61956.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; soluble; CD23; complementarity determining;
isoform B; recombinant production.
          IgE binding factor
                             04-FEB-1991
                                                                                                                                                                                                                                                                                                                                                                                                                             28-DEC-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                               27-DEC-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   04-FEB-1997.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       JP09028385-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17-JUN-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAW13143;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAW13143 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence containing human soluble CD23 isoform B.
                                                                                                                    95
                                                                                                                                                                  Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             58
                                                                                                                                     2 RAEQQRLKSQDL 13
                                                                                                                   RAEQQRLKSQDL 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RAEQQRLKSQDL 69
                                                                                                                                                         1 Similarity
12; Conserv
                                                                                                                                                                                                320 AA;
                                                                                                                                                          Conservative
                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                              94US-0365103
                                                                                                                                                                                                                                                                                                                                                                                                                                                 95JP-0341169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                  protein;
                                                                                                                                                      91.9%; suc
100.0%; Pr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "soluble CD23 isoform
                                                                   321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             320
                                                                                                                                                                  Score 57;
Pred. No.
                                                                   ⋛
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8
                                                                                                                                                         Mismatches
                                                                                                                                                                  0.1
                                                                                                                                                                                                                                                                                                                              of CD23 -
                                                                                                                                                                  в 18;
.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           B
                                                                                                                                                          0
                                                                                                                                                                           Length 320;
                                                                                                                                                                                                                                                                                                                             useful for large
                                                                                                                                                          Indels
                                                                                                                                                          0
                                                                                                                                                          Gaps
                                                                                                                                                          0
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RESULT 5
AAP82073
ID AAP8
XX AAP82073
AC AAP8
XX LOW
XX LO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
""" hes 12; Conserv?
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DЬ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30-APR-1986;
04-SEP-1986;
05-SEP-1986;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The protein reacts with anti-Fc epsilon receptor antibody, and is obtd. in large quantities. The DNA encoding the protein is obtd. from, eg human B cells, human malignant B or T cells, human monocytes or human eosinophilic cells. RRMI 8866 cells may also be cultured to produce the mRNA. The IgE binding factor and Fc epsilon receptor binds IgE and can be used to enhance the produc. They can be used to treat allergies by eliminating excess blood IgE, and can also
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New IgE binding factor protein - obtd. by cu class specific Fc receptor on their surface.
   Cleavage-site
                                                                                                                                                                                                                                                                                                                                          17-OCT-1990
                                                                                                                                                                                                                                                                                                                                                                         AAP82073;
                                                                                                                                                                                                                                                                                                                                                                                                       AAP82073 standard; protein; 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 6; page 42-3; 57pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-PSDB; AAN70107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Honjo T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         29-APR-1987;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         09-DEC-1987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
                                                  Modified-site
                                                                                                  Domain
                                                                                                                                                              Domain
                                                                                                                                                                                                                                                                          Low affinity Fc
                                                                                                                                                                                                                                                                                                          Recombinant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (KURS ) KURARAY CO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IgE binding
                                                                                                                                                                                              Domain
                                                                                                                                                                                                                                           Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    96 RAEQQRLKSQDL 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 RAEQORLKSQDL 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1987-343202/49.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Yodoi J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    321 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        factor;
                                                                                                                                                                                                                                                                                                        Fc_epsilon receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          86JP-0101531.
86JP-0209091.
86JP-0210429.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         87EP-0106265
                                                                                                                                                                                                                                                                         epsilon
 /note="N-linked"
149..150
                                                                                                            /label-stop_transfer_seg
/note-"basic cluster involved
integration into bilayer"
                                                                                                                                                                                                           Location/Qualifiers
                                                             /label-transmembrane region
/note-"hydrophobic residues"
                                                                                                                                                                           note-"hydrophilic N-terminal"
                                 label=glycosylation_site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  91.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Takami
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       epsilon receptor; allergy; RPMI 8866 cells;
                                                                                                                                                                                                                                                                          receptor; IgE; allergy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Z
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 57;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                       Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           culturing cells harbouring a
                                                                                                                              in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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밁
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1988-065437/10.
P-PSDB; AAP82073.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Kishimoto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23-SEP-1986;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          09-MAR-1988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EP258489-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Protein
                               WPI; 1988-057531/09
N-PSDB; AAN81485.
                                                                                                                                                                                                                                                                                                                                     Low affinity
                                                                                                                                                                                                                                                                                                                                                                                                      AAP81163;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
 New human lower affinity Fc(epsilon)-receptor - useful for treating
                                                                                Kishimoto T,
                                                                                                            (KISH/) KISHIMOTO T.
                                                                                                                                            21-AUG-1986;
                                                                                                                                                                           21-AUG-1986;
                                                                                                                                                                                                           02-MAR-1988
                                                                                                                                                                                                                                           EP257114-A.
                                                                                                                                                                                                                                                                          Ното
                                                                                                                                                                                                                                                                                                       Low affinity
                                                                                                                                                                                                                                                                                                                                                                        15-OCT-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21-AUG-1986;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  96 RAEQQRLKSQDL 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 RAEQQRLKSQDL 13
                                                                                                                                                                                                                                                                         sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   l similarity
12; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ŧ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 321
                                                                                Suemura
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AA;
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New human low affinity Fc(epsilon)-receptor and parts for treating local or systemic allergic reactions and recombinant DNA methods.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DNA encoding the sequence or a part of it can be used to make recombinant receptor which is useful for treating IgE allerg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 4; Page 39; 59pp; English.
                                                                                                                                                                                                                                                                                                                                                 AAP81163 standard; protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (CELL-) CELLULAR IMMUNOLOGY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                     Fc_epsilon receptor; IgE; allergy.
                                                                                                                                                                                                                                                    Fc_epsilon receptor
                                                                                                                                                                                                                                                                                    (first entry)
                                                           86EP-0111581
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Suemura M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    86EP-0111581
                                                                                          86EP-0111581
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    86EP-0113073
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/note="Claim 7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                150..150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /label-membrane_bound
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="target for trypsin-like proteases"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            91.9%;
ž
Kikutani H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kikutani H,
                                                                                                                                                                                                                                                                                                                                                    321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 57;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                   Ą
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                    encoded by gene carried by pGEM4.
Barsumian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Barsumian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 321
E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IgE allergic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       - useful
obtd. by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9
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ARESULT 7

AAAB1230

ID AAAB

XX AAAB

XX AAAB

XX Z5-0

DT 25-0

DX FC G

XX FC G

XX FC G

XX JP63

PN JP63

PN JP63

PN JP63

PN UP63

XX V4-A

XX V4-A

XX VAT

PT FOF

PT FOF

PT FOF

XX PF G

XX PF G

XX CT

 RESULT 8
AAP81112
ID AAP8
XX
AC AAP8
AC AAP8
XX
DT 12-D
XX
Huma
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Best Local S
Matches 12
                                                                                                                                                                                                                                      Query Match 91.9
Best Local Similarity 100
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                              FC epsilon receptor binds IgE. It is each it is expressed in large amts, and can blood, and to detect and quantify IgE. of therapy and diagnosis of allergy.
Human IgE binding factor related polypeptide.
                                  12-DEC-1990
                                                               AAP81112;
                                                                                              AAP81112 standard;
                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; ge 529; 16pp; japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                           New DNA contg. nucleotide sequence encoding Fc epsilon receptor for obtaining IgE-binding substance used to detect and quantify IgE responsible for allergies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1988-273895/39
N-PSDB; AAN81612.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   05-SEP-1986;
24-APR-1987;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 24-APR-1987;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               17-AUG-1988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              JP63198988-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Fc epsilon receptor; IgE; allergy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Fc gamma receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAP81230 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     local and allergic reactions produced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (KURS ) KURARAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         25-OCT-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAP81230;
                                                                                                                                                                            96 RAEQORLKSQDL 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   96
                                                                                                                                                                                                           N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 RAEQQRLKSQDL 13
                                                                                                                                                                                                           RAEQQRLKSQDL 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RAEQORLKSODL 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Page 24;
                                                                                                                                                                                                                                                                                                    321 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           321 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first
                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   86JP-0210429
87US-0042445
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ξ.
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                                                                                            peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    protein;
                                                                                                                                                                                                                                   91.9%; 5c.
100.0%; Pr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            91.98;
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                                                                                               321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     321
                                                                                                                                                                                                                                        Score 57; DB; Pred. No. 0.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 57;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ⋛
                                                                                               8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                expressed from cell line RPMI8866.

n be used to remove excess IgE from
this would allow the development
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      by the
                                                                                                                                                                                                                                                      DB 9;
0.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 9;
0.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      expression of IgE
                                                                                                                                                                                                                                         0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
                                                                                                                                                                                                                                                                   Length 321;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 321;
                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              indels
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                                                                                                                                                                                                                                        0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0
                                                                                                                                                                                                                                                                                                                                                              RESULT 9
AAP81172
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Best Local :
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 11-APR-1987;
21-AUG-1986;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                    AAP81172;
                                                                                                                                                                        therapy.
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The peptide is related to the IgE receptors on human B-cells and, if without the membrane anchoring sequence, to the IgE-BFs of Sarfati et al. Immunology 53, 197, 207, 783 (1984).

Amino acids between 1-133 starting from the N-terminal may be deleted. This is the membrane-anchoring sequence binding the polypeptide to the Cytoplasmic membrane of the B-cells.

Alternatively amino acids between 110-130 or 250-321 may also be deleted. The peptide has IgE binding activity and is useful tor treating allergic conditions, e.g. as caused by antigens such as pollens,
                                                            06-AUG-1987;
                                                                                                                                                                                                                                                                                          Sequence encoded by a gene for the water-soluble part of the human low affinity Fc-epsilon-receptor with the amino acids 150 to 321, comprising the EcoRI insert from pFc-epsilon-R-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; Page 36; 48pp;
                                                                                                      16-MAR-1988.
                                                                                                                                               EP259615-A.
                                                                                                                                                                                                                                                                                                                                                                                 28-MAR-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAP81172 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cat danders and house dust mites.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New IgE binding factor related polypeptide(s) - produced by recombinant methods.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-PSDB; AAN81437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1988-022917/04.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hofstetter H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  22-JUL-1986;
07-NOV-1986;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20-JUL-1987;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human IgE binding factor; IgE-BFs; allergic diseases; B-cells
                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                 ow affinity Fc-epsilon-receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (CIBA ) CIBA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     96 RAEQORLKSODL 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity es 12; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 RAEQQRLKSQDL 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        321 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GEIGY AG
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87EP-0105425
86EP-0111581
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86GB-0026622
                                                              87EP-0111392
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               91.9%; 5r
100.0%; Pr
0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   321
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                     systemic IgE-allergic reaction;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 9;
0.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 321;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0
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RESULT 10
AAP90120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The inventors claim a human low affinity Fc-epsilon-receptor (FCR)

With an N-terminal cytoplasmic domain, a C-terminal extracellular

domain and a mol.wt. of about 46kd. Also claimed are recombinant DNA

contg. the genetic information for the FCR, vectors contg. the DNA,

host organisms transformed with the vectors, oligonucleotides coding

for partial amino acid sequences from FCR, and processes for

preparing FCR. Preferred embodiments of the present invention are

preparing FCR. Preferred embodiments of the present invention are

part of the cDNA SQ coding for the ANS 1 to 148 of the Fc-epsilon-R

is replaced by a eucaryotic cDNA signal SQ e.g. an interlewin cDNA

signal SQ e.g.by the BSF-2 signal SQ (see pBSF-2-L8-AAN81517/P81176).

A suitable yeast expression vector is a plasmid contg. the yeast

ADHI-promoter, a gene coding for the yeast mating factor alpha

leader peptide (MF alpha leader SQ) a multicloning site and the

yeast ADHI-terminator (see AAN81514/P81173). See also EP-258492.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local :
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05-DEC-1986;
06-AUG-1987;
                                                    Kishimoto T,
Schwendenwein
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human lymphocyte receptor asthma; immunoglobulin E;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-NOV-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Recombinant human low affinity Fc(epsilon)- receptor - used for the treatment of local and systemic IGE-allergic reactions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Kishimoto T,
  WPI; 1989-214148/30.
                                                                                                                                                                                      20-JAN-1988;
                                                                                                                                                                                                                                        20-JAN-1988;
                                                                                                                                                                                                                                                                                             26-JUL-1989
                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human lymphocyte receptor for immunoglobulin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAP90120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAP90120 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-PSDB; AAN81512
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   96 RAEQQRLKSQDL 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 RAEQQRLKSQDL 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1988-072124/11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      l Similarity
12; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Table 3, Page 79-81; 118pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                321 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry
                                                                                                                                                                                                                                                                                                                                                                                                      (Human)
                                            Suemura M, Kikutani H, Bar
R, Sommergruber W, Swetly
                                                                                                                                  UNIVERSITY.
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86EP-0116938.
87EP-0111392.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     lymphocyte
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           for immunoglobulin; hypersensitivity; allergy;
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Pred. No.
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Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        receptor
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                                                 Barsumian
tly P;
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                                                                             Schneider F-J;
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RESULT 11
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                                                                                  Matches
                                                                                                                          Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Soluble recombinant Fc-epsilon receptor - used for treatment or prophylaxis of local and allergic reactions induced by IgE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Whole human lymphocyte receptor for immunoglobulin (see corres AAN90344). Used to produce highly bloactive water-soluble FCR. Water-soluble FCR binds 1gE, so it is useful for treating hypersensitivity, esp. asthma. Amino acid residue 150 is a possible site for trypsin-like proteases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-PSDB; AAN90344.
                                                                                                                                                                                                                                                                                                                                                                                                                             Kishimoto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; fig 1; 23pp; English.
                                                                                                                                                                     Sequence
                                                                                                                                                                                                             The known
                                                                                                                                                                                                                                                        Disclosure;
                                                                                                                                                                                                                                                                                                Cloned genes coding for soluble IgE receptor - coding sequence of Fc epsilon receptor gene.
                                                                                                                                                                                                                                                                                                                                                              N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1989-186101/26.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (OSAU ) OSAKA UNIVERSITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    22-DEC-1987;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            22-DEC-1987;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     28-JUN-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EP321601-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Fc epsilon
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96
                                                                                                      Local
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                                        RAEQQRLKSQDL
RAEQQRLKSQDL
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                                                                                  l Similarity
12; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sequence of
                                                                                                                                                                                                                                                                                                                                                              AAN90134, AAN90135, AAN90136
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                                                                                                                                                                                                             peptide sequence of Fc
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                                                                                                                                                                     321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     receptor; cloned gene; IgE; allergy; ,asthma
                                                                                                                                                                                                                                                     fig 1; 19pp;
                                                                                  Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                             Suemura M,
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107
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                                                                                                      91.9%;
                                                                                                                                                                                                                                                        English.
                                                                                                                                                                                                                                                                                                                                                                                                                               Kikutani H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 57; Pred. No.
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                                                                                                    DB 10;
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RESULT 12 AAR42053 ID AAR42

AAR42053 standard; Protein; 321 AA.

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RESULT 13
AAW13142
ID AAW13
XX
AC AAW13
XX
DT 17-JU
XX
E Seque
XX
Human
KW Human
KW Homo
XX
Homo
XX
PFT Pept!
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PR
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PF 37-D
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Best Local S
Matches 12
                    04-FEB-1997
                                                                                                                                       Sequence containing human soluble CD23 isoform A.
                                                                                                                                                            17-JUN-1997
                                                                                                                                                                             AAW13142;
                                                                                                                                                                                             AAW13142 standard;
                                                                                                                                                                                                                                                                                                                                    The sequence is of IgE-binding factor, secreted from the plasmid pSVG-BF. The plasmid pSVG-BF is a derivative of plasmid pSVG-ER which has the sequence coding amino acids 1-147 replaced with a coding region (AAQS5400) allowing secretion of the factor.
                                                                                                                                                                                                                                                                                                                                                                                                   Recombinant DNA molecule - comprises enhancer and promoter unit linked to transcriptive DNA segment and DNA segment comprising promoter unit linked to DNA sub-segment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Key
Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IgE;
27-DEC-1995;
                                     JP09028385-A
                                                                Peptide
                                                                                                                       Human; soluble;
                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1993-275121/35.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               03-DEC-1987;
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                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Page 28; 71pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IL84702-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IgE binding
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                                                                                                             isoform A;
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                                                                                                                                                                                                                                                     RAEQQRLKSQDL 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           binding
                                                                                          sapiens
                                                                                                                                                                                                                                           RAEQQRLKSQDL 107
                                                                                                                                                                                                                                                                              l Similarity 100 12; Conservative
                                                                                                            recombinant
                                                                                                                                                                                                                                                                                                                    321 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            factor.
                                                                                                                                                          (first
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           factor; secretion;
95JP-0341169.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             87IL-0084702
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               871L-0084702
                                                                                                                       CD23;
                                                               Location/Qualifiers
1..205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                       /note-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /label=
                                                                                                                                                                                              Protein;
                                                                                                                                                         entry)
                                                                                                                                                                                                                                                                                        91.9%;
                                                                                                            complementarity determining; t production.
                                                      "soluble CD23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IgE-binding_factor
                                                                                                                                                                                                                                                                                        .08:
                                                                                                                                                                                              321
                                                                                                                                                                                                                                                                               0;
                                                                                                                                                                                                                                                                                        Score 57;
                                                                                                                                                                                              ξ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           expression; signal sequence.
                                                                                                                                                                                                                                                                             Mismatches
                                                       isoform
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0.1;
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                                                                                                                                                                                                                                                                                                Length 321;
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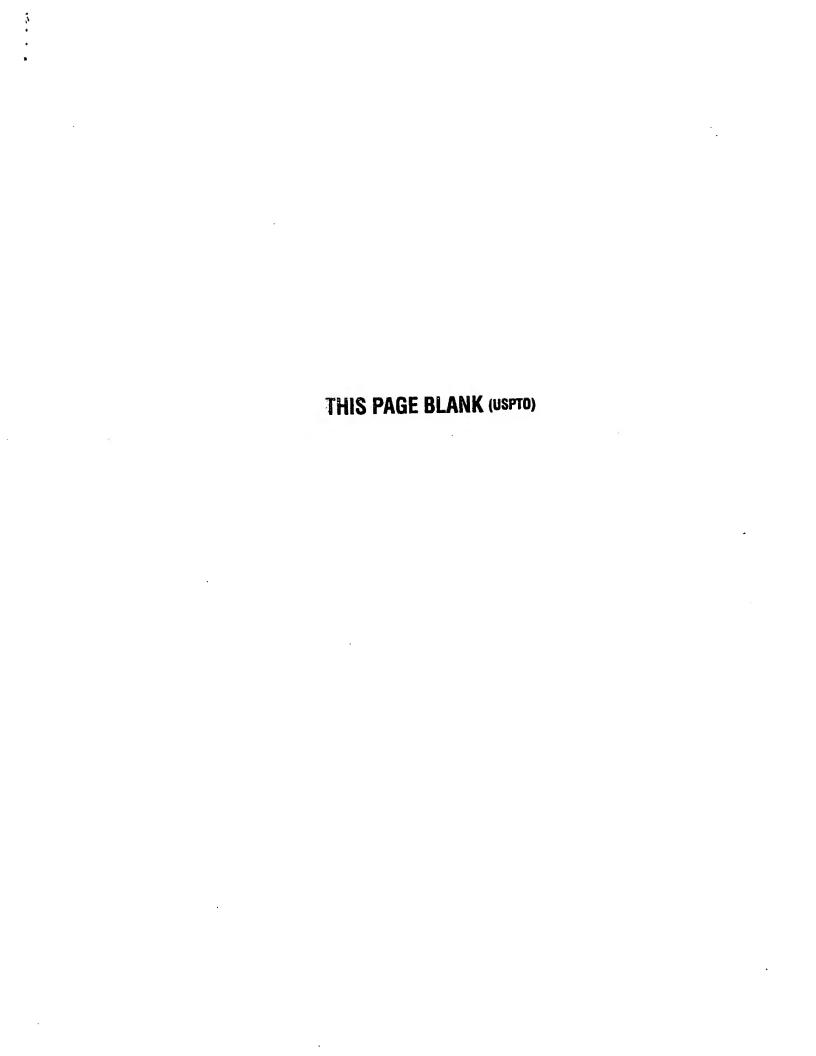
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AAP82839
ID AAP82839
ID AAP82839
ID AAP82839
AC AAP82
XX AAP82
XX I6-NO
DT 16-NO
DX Human
XX FC(ep
XX FC(ep
XX FC(ep
XX FC(ep
XX FC(ep
I EP258
XX O5-DE
XX O5-DE
XX K1sh1
XX K1sh1
XX WPI;
DR WPI;
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (LYNC/) LYNCH R G. (MATS/) MATSUI M. (NUNE/) NUNEZ R M. (YODO/) YODOI J.
             This protein is useful in the treatment of local or systemic IgE-allergic reactions and is obtd. by recombinant DNA methods. It ipref. un-accompanied by associated native glycosylation. Fragments it can also be used. See also AAN82253.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The cDNA encoding the present sequence, which contains human soluble CD23 isoform A, can be used for the large scale recombinant production of soluble CD23.

The specification states that the nucleotide sequences contained in figures 4a-b, 5a-b, 12a-12b and 13a-b are claimed, however this numbering scheme does not relate to the scheme used in the relevant
                                                                            Disclosure; ; pp;
                                                                                                     New human low affinity Fc(epsilon)-receptor and parts treating local or systemic IgE-allergic reactions and recombinant DNA methods.
                                                                                                                                                                                                Kishimoto T,
                                                                                                                                                                                                                                                    05-DEC-1986;
                                                                                                                                                                                                                                                                           05-DEC-1986;
                                                                                                                                                                                                                                                                                                     09-MAR-1988
                                                                                                                                                                                                                                                                                                                             EP258492-A.
                                                                                                                                                                                                                                                                                                                                                       Fc(epsilon) receptor; low affinity; IgE-allergic reactions
                                                                                                                                                                                                                                                                                                                                                                                 Human low affinity Fc(epsilon) receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                    AAP82839;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAP82839 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         in figures 4a-b, 5a-b, 12a-12b and 1 numbering scheme does not relate to sections of the specification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; Pages 16-17; 33pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DNA sequence encoding a soluble isoform scale preparation of the protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1997-159094/15
N-PSDB; AAT61955.
                                                                                                                                                          N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                          16-NOV-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                          (CELL-) CELLULAR IMMUNOLOGY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        28-DEC-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               96
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                                                                                                                                                          1988-065440/10.
DB; AAN82252.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    321 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
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                                                                                                                                                                                                Suemura
                                                                                                                                                                                                                                                  86EP-0116938
                                                                                                                                                                                                                                                                            86EP-0116938
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                                                                            English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            91.9%;
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                                                                                                                                                                                                Kikutani
                                                                                                                                                                                                                                                                                                                                                                                                                                                              336
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 57;
Pred. No.
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ents of
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Job time : 35.5091 secs

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RESULT 15
AAP83022
ID AAP83
AX AAP83
XX AAP83
XX AAP83
XX AAP83
XX Human
XX Human
XX Human
XX Homo
XX F25-JU
PR 07-NO
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Search completed: March 13, 2003, 18:49:15
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Best Local S
Matches 11
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Best Local Similarity
Matches 12; Conserv
                                                                                                                                                                                                                                                                                                                                                         The cDNA is obtained by reverse transcription of mRNA isolated from cells expressing IgE-binding activity, esp. human B-cells RPMI 8866. The peptide is related to the IgE receptors on human B-cells and, if without the membrane anchoring sequence, to the IgE-BFs of Sarfati et al. Immunology 53, 197, 207, 783 (1984). Amino acids between 1-133 starting from the N-terminal may be deleted. This is the membrane-anchoring sequence binding the polypeptide to the cytoplasmic membrane of the B-cells.

Alternatively amino acids between 110-130 or 250-321 may also be deleted. The peptide has IgE binding activity and is useful tor treating allergic conditions, e.g. as caused by antigens such as pollens, cat danders and house dust mites.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  22-JUL-1986;
07-NOV-1986;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EP254249-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human IgE binding factor; IgE-BFs; allergic diseases; pCL-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human IgE binding factor related polypeptide from pCL-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAP83022;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAP83022 standard; protein; 300 AA.
                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The sequence has the formula of AAP81112\ wherein the amino acids 106\text{-}127\ are\ deleted.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; ; 48pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    recombinant methods.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New IgE binding factor related polypeptide(s) - produced by DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N-PSDB; AAN81438.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hofstetter H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (CIBA ) CIBA GEIGY AG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20-JUL-1987;
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                                                                                       96
                                                                                                                                                                                               Local Similarity 91.7 les 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     96 RAEQQRLKSQDL 107
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                                                                                                                                           2 RAEQQRLKSQDL 13
                                                                                    RAEQQRLKSQEL 107
                                                                                                                                                                                                                                                                                                          300 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              336 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kilchherr E;
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86GB-0026622.
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                                                                                                                                                                                                                      85.5%;
91.7%;
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Pred. No. 0.44;
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Compugen Ltd.
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37	37	37	37	37	37	37	37	37	37	37	37	38	38	38	38
59.7	59.7	59.7	59.7	59.7	59.7	59.7	59.7	59.7	59.7	59.7	59.7	61.3	61.3	61.3	61.3
758	495	462	461	383	317	312	301	196	182	174	77	1534	1270	938	460
N	ν	N	ν	N	2	N	N	N	N	N	ν	N	N	N	2
F75590	T20754	A46170	S50864	G84597	JC7207	S53969	T32803	C82056	F97928	A95060	E69894	A56734	T09194	A56731	F84529
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ALIGNMENTS

22 40 64.5 248 2 \$10623 tropomyosin 4, fib 23 39 62.9 278 1 TPHUTW troponin T, slow s 24 39 62.9 309 1 \$34198 IgE Fc receptor II 25 39 62.9 1691 1 A44212 genome polyprotein 26 38 61.3 146 2 F82418 cytochrome c554 VC 27 30 61.3 146 2 F82418 cytochrome c554 VC	41 66.1 297 2 B44781 troponin T, car 41 66.1 298 1 TPHUTC troponin T, car 41 66.1 299 2 S30443 troponin T - ra	41 bb.1 2/2 A24824 troponin T, 41 66.1 274 2 A31957 troponin T, 41 66.1 284 2 A28008 troponin T, 41 66.1 289 2 A44781 troponin T,	66.1 258 2 153021 troponin T - 66.1 263 2 C31957 troponin T, 66.1 266 1 TPRBTS troponin T,	41 66.1 253 2 41 66.1 257 2	41 66.1 249 2 A444459 troponin T, 41 66.1 250 2 S48793 troponin T,	66.1 175 2 66.1 234 2 66.1 249 2	3/ 91.9 3/1 1 LNHUEK 19E FC recep 44 71.0 302 1 TPCHTC troppoin T 43 69.4 756 2 E75590 methyl-accep	Score Match Length DB ID Description	sult Query	Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.	2: pir2:* 3: pir3:* 4: pir4:*	IR_73:* pir1:*	st-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries	nimum DB seq length: 0 ximum DB seq length: 2000000000	tal number of hits satisfying chosen parameters: 283224	arched: 283224 segs, 96134422 residues	oring table: BLOSUM62 Gapop 10.0 , Gapext 0.5	tle: US-10-050-200-7 rfect score: 62 quence: 1 ERAEQQRLKSQDL 13	n on: March 13, 2003, 18:46:17; Search time 12.7636 Seconds (without alignments) 97.915 Million cell updates/sec
A; Molecule type: mRNA A; Residues: 1-268, 'T', 270-321 <lud> A; Residues: 1-268, 'T', 270-321 <lud> A; Residues: 1-268, 'T', 270-321 <lud> A; Cross-references: GB:X04772; NID:g34002; PIDN:CAA28465.1; PID:g34003 A; Note: the codon given for 269-Asn (ACC) is inconsistent with the authors' translati A; Note: part of this sequence, including the amino end of soluble forms of the protei A; Note: part of this sequence, including the amino end of soluble forms of the protei R; Ikuta, K.; Takami, M.; Kim, C.W.; Honjo, T.; Miyoshi, T.; Tagaya, Y.; Kawabe, T.; Y Proc. Natl. Acad. Sci. U.S.A. 84, 819-823, 1987 A:Title: Human lymphocyte Fc recentor for IGE: sequence homology of its cloned conA w</lud></lud></lud>	A;Title: Cloning and expression of the cDNA coding for a human lymphocyte A;Reference number: A26164; MUID:87218454; PMID:3034567 A;Accession: A26164	A; Residues: 'MNPPSQD', 47-50 <masz> A; Experimental source: splice form b' R; Ludin, C.; Hofstetter, H.; Sarfati, M.; Levy, C</masz>	A; Experimental source: splice form a' A; Accession: S39443 A; Molecule type: DNA	A; ACCESSION: S39442 A; MOIGCULE type: DNA A; Residues: 1-7,'D',47-50 <mas1></mas1>	A; Title: Alternative transcripts of the human CD23/Fc-epsilon-RII. A; Reference number: S39442; MUID:94063078; PMID:8243664	` Ω		A; Accession: S03279 A; Status: nucleic acid sequence not shown; not compared with conceptual translation	Nucleic Actus Res. 15, /25-/308, 198/ A;Title: Molecular structure of the gene and the 5'-flanking A;Reference number: S03279; MIID:88015506; PMID:2958779	A; Residues: 1-321 <kik> A; Residues: 1-321 <kik> A; Cross-references: GB:M14766; NID:g182449; PIDN:AAA52435.1; PID:g182450 A; Experimental source: EBV-transformed B lymphoblastoid cells RPMI-8866 R; Suter, U.; Bastos, R.; Hofstetter, H.</kik></kik>	A;Title: Molecular structure of human lymphocyte receptor for immunoglobulin E. A;Reference number: A26067; MUID:87051737; PMID:2877743 A;Accession: A26067 A;Accession: A26067	C;Accession: A26067; S03279; S39442; S39443; A26164; A26589; A31924; JL0132; R;Kikutani, H.; Inui, S.; Sato, R.; Barsumian, E.L.; Owaki, H.; Yamasaki, K.; Cell 47, 657-665, 1986	N;Contains: 19E Fc receptor II, splice form a; IgE Fc receptor II, splice C;Species: Homo sapiens (man) C;Date: 31-Mar-1988 *sequence revision 31-Mar-1988 *text_change 15-Sep-200	receptor II	RESULT 1	ALIGNMENTS	59.7 758	1 37 59.7 383 2 2 37 59.7 461 2 3 37 59.7 462 2	37 59.7 196 2 37 59.7 301 2 37 59.7 312 2
AA28465.1; PID:g34003 Insistent with the author oend of soluble forms yoshi, T.; Tagaya, Y.;	for a human lympho)34567	C.A.; Suter, U.; Alaimo, D.;			3/Fc-epsilon-RII. A possible 243664	but the complete sequence is R.G.; Yodoi, J.		mpared with conceptua	o'-flanking region of 158779	WA52435.1; PID:g1824 estoid cells RPMI-886	receptor for immunogl 377743	4; A26589; Å31924; JL0132; S .; Owaki, H.; Yamasaki, K.;	Fc receptor II, spl #text_change 15-Sep	lan			methyl-accepting c	probable XAP-5 pro probable XAP-5 pro avermectin-sensiti tektin Al - sea ur	probable NAD(P)H o hypothetical prote hypothetical prote

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A;UTOSB*TETELERICES. VALLED CONTROLL AND POSITION: 1913 3-1913.3 1913.3 1913.3 1913.3 1913.3 1913.3 1913.3 1913.3 1913.3 1913.3 1913.3 1913.3 1913.3 1913.3 1913.3 1913.3 1913.3 1913.3 1913.3 1913.3 1913.3 1913.3 1913.3 1913.3 1913.3 1913.3 1913.3 1913.3 1913.3 1913.3 1913.3 1913.3 1913.3 1913.3 1913.3 1913.3 1913.3 1913.3 1913.3 1913.3 1913.3 1913.3 1913.3 1913.3 1913.3 1913.3 1913.3 1913.3 1913.3 1913.3 1913.3 1913.3 1913.3 1913.3 1913.3 1913.3 1913.3 1913.3 1913.3 1913.3 1913.3 1913.3 1913.3 1913.3 1913.3 1913.3 1913.3 1913.3 1913.3 1913.3 1913.3 1913.3 1913.3 1913.3 1913.3 1913.3 1913.3 1913.3 1913.3 1913.3 1913.3 1913.3 1913.3 1913.3 1913.3 1913.3 1913.3 1913.3 1913.3 1913.3 1913.3 1913.3 1913.3 1913.3 1913.3 1913.3 1913.3 1913.3 1913.3 1913.3 1913.3 1913.3 1913.3 1913.3 1913.3 1913.3 1913.3 1913.3 1913.3 1913.3 1913.3 1913.3 1913.3 1913.3 1913.3 1913.3 1913.3 1913.3 1913.3 1913.3 1913.3 1913.3 1913.3 1913.3 1913.3 1913.3 1913.3 1913.3 1913.3 1913.3 1913.3 1913.3 1913.3 1913.3 1913.3 1913.3 1913.3 1913.3 1913.3 1913.3 1913.3 1913.3 1913.3 1913.3 1913.3 1913.3 1913.3 1913.3 1913.3 1913.3 1913.3 1913.3 1913.3 1913.3 1913.3 1913.3 1913.3 1913.3 1913.3 1913.3 1913.3 1913.3 1913.3 1913.3 1913.3 1913.3 1913.3 1913.3 1913.3 1913.3 1913.3 1913.3 1913.3 1913.3 1913.3 1913.3 1913.3 1913.3 1913.3 1913.3 1913.3 1913.3 1913.3 1913.3 1913.3 1913.3 1913.3 1913.3 1913.3 1913.3 1913.3 1913.3 1913.3 1913.3 1913.3 1913.3 1913.3 1913.3 1913.3 1913.3 1913.3 1913.3 1913.3 1913.3 1913.3 1913.3 1913.3 1913.3 1913.3 1913.3 1913.3 1913.3 1913.3 1913.3 1913.3 1913.3 1913.3 1913.3 1913.3 1913.3 1913.3 1913.3 1913.3 1913.3 1913.3 1913.3 1913.3 1913.3 1913.3 1913.3 1913.3 1913.3 1913.3 1913.3 1913.3 1913.3 1913.3 1913.3 1913.3 1913.3 1913.3 1913.3 1913.3 1913.3 1913.3 1913.3 1913.3 1913.3 1913.3 1913.3 1913.3 1913.3 1913.3 1913.3 1913.3 1913.3 1913.3 1913.3 1913.3 1913.3 1913.3 1913.3 1913.3 1913.3 1913.3 1913.3 1913.3 1913.3 1913.3 1913.3 1913.3 1913.3 1913.3 1913.3 1913.3 1913.3 1913.3 1913.3 1913.3 1913.3 1913.3 1913.3 1913.3 1913.3 
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A;Reference number: A65963; PDB:1KTE
A;Contents: annotation; conformation by theoretical model, residues 173-285
C;Comment: The sequence of the splice form a is shown.
C;Comment: This receptor for the Fc portion of IgE is expressed in various hematopoietic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Experimental source: lymphoblastoid B cell line R; Rose, K.; Turcatti, G.; Graber, P.; Pochon, S.; Regamey, P.O.; Jansen, K.U.; M Biochem, J. 286, 819-824, 1992

A; Title: Partial characterization of natural and recombinant human soluble CD23. A; Reference number: $29107; MUID:93038513; PMID:1417742
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Molecule type: mRNA
A;ResIdues: 'MNPPSQ', AB-14 <YOK>
A;ResIdues: 'MNPPSQ', AB-14 <YOK>
A;Cross-references: GB:M23562; NID:g182444
A;Experimental source: splice form IIb
R;Letellier, M.; Sarfati, M.; Delespesse, G.
Mol. Immunol. 26, 1105-1112, 1989
A;Title: Mechanisms of formation of IgE-binding factors (soluble CD23)-I.
A;Reference number: JL0132; MUID:90220658; PMID:2534424
A;Accession: JL0132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Comment: Splice form a is expressed constitutively in B-cells; b is expressed in C;Comment: Soluble IgE-binding factors are produced by proteolytic cleavage of IgE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          submitted to the Brookhaven Protein Data Bank, June 1993 A;Reference number: A51791; PDB:1HLI A;Contents: annotation; conformation by theoretical model, residues 173-285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Title: Two species of human A;Reference number: A31924; Mt A;Accession: A31924
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Reference number: A26589;
A;Accession: A26589
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: GDB:118888; OMIM:151445
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Gene: GDB:FCER2; FCE2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C; Genetics:
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A; Residues: 152-166; 173-179; 189-212; 230-263; 268-306
R; Padlan, E.A.; Helm, B.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Reference number: $29107;
A; Accession: $29107
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MUID:89028672; PMID:2972386
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Fc re
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Matches
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Query

Match

91.9%;

Score 57;

DB 1;

Length 321;

Local

2

Indels

0;

Gaps

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A;Title: A single troponin T gene regulated by different programs in cardiac A;Reference number: A03086; MUID:85065747; PMID:6095446
A;Receasion: A03086
A;Molecule type: mRNA
A;Residues: 68-302 <CCO2>
A;Cross-references: GB:K02263; NID:g212781; PIDN:AAA49098.1; PID:g212782
A;Cross-references: GB:K02263; NID:g212781; PIDN:AAA49098.1; PID:g212782
C;Comment: This protein, found in adult cardiac muscle and translently in emb and skeletal muscle. Down-regulation of the protein in the late stages of ske
                                                                                                                                        A; Experimental source: C; Genetics:
                                                                                                                                                                                                                                                  S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999
S,Title: Genome sequence of the radioresistant bacterium A;Reference number: A75250; MUID:20036896; PMID:10567266
A;Accession: E75590
A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                     methyl-accepting chemotaxis-related protein - Delnococcus radiodurans (strain C;Species: Delnococcus radiodurans C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 31-Mar-2000 C;Accession: E75590
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R;Cooper, T.A.; Ordahl, C.P.
J. Biol. Chem. 260, 11140-11148, 1985
A;Title: A single cardiac troponin T gene generates embryonic A;Reference number: A25373; MUID:85289327; PMID:2993302
A;Accession: A25373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       troponin T, cardiac muscle, embryonic splice form - chicken N;Contains: cardiac muscle troponin T, adult splice form C;Species: Gallus gallus (chicken) C;Date: 28-Aug-1985 *sequence_revision 12-Apr-1996 *text_change C;Accession: A25373; A03086
                                                                                                                                                                A; Molecule type: DNA
A; Residues: 1-756 <WHI>
                                                                                                                                                                                                                                                                                                                                                                   R;White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
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C; Keywords: alternative splicing; cardiac muscle; differentiation; heart; muscle;
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Science 226, 979-982,
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h 69.4%;
Similarity 69.2%;
9; Conservative
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72.7%;
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Pred. No.
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troponin T, fast skeletal muscle splice form alpha - rabbit (frac C; Species: Oryctolagus cuniculus (domestic rabbit) C; Date: 30-Apr-1993 #sequence_revision 17-May-1996 #text_change 1 C; Accession: B44459 R; Pan, B.S.; Potter, J.D.
J. Biol. Chem. 267, 23052-23056, 1992
A; Title: Two genetically expressed troponin T fragments represent A; Reference number: A44459; MUID:93054628; PMID:1429653 A; Accession: B44459
A; Status: nucleic acid sequence not shown; not compared with cond A; Molecule type: mRNA A; Residues; 1-234 <PAN>
A; Residues; 1-234 <PAN>
A; Experimental source: neonatal skeletal muscle clone pT7 A; Note: sequence extracted from NCBI backbone (NCBIP:118207) C; Comment: The two carboxyl-terminal isoforms of troponin T are cexpression of troponin T.
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A; Cross references: EMBL:
C; Genetics:
A; Introns: 14/2
C; Superfamily: troponin T
C; Keywords: cardiac muscl
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A34327
A34327
A34327
C:Species: Coturnix coturnix japonica (Japanese quail)
C:Date: 22-Jun-1990 *sequence_revision 22-Jun-1990 *text_change C;Accession: A34327
C;Accession: A34327
C;Accession: Chem. 264, 12482-12491, 1989
A;Title: Developmental and muscle-specific regulation of avian fa;Reference number: A34327; MUID:89308680; PMID:2745456
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S48795
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C;Keywords: alternative splicing; differentiation; skeletal muscle
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ferences: EMBL:X79859;
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A; Molecule type: mRNA
A; Residues: 1-249 < PANA
A; Note: sequence extracted from NCBI backbone (NCBIP:118206)
A; Note: sequence extracted from NCBI backbone (NCBIP:118206)
A; Putney, S. D.; Herlihy, W.C.; Schimmel, P.
Nature 302, 718-721, 1983
A; Title: A new troponin T and cDNA clones for 13 different muscle proteins,
A; Reference number: 146471; MUID:83167564; PMID:6687628
A; Accession: 146517
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     troponin T, fast skeletal muscle splice form beta .C;Species: Oryctolagus cuniculus (domestic rabbit) C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 C;Accession: A44459; 146517 R;Pan, B.S.; Potter, J.D.
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A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-249 <BUC>
A;Cross-references: GB:M26599; NID:g213627;
C;Superfamily: troponin T
C;Keywords: skeletal muscle
A; Molecule type: mRNA
A; Residues: 1-250 <FAR>
A; Cross-references: EMBL:X79861; NID:g587427;
C; Superfamily: troponin T
C; Keywords: cardiac muscle; heart
                                                                                                                                                                                                                         troponin T, cardiac muscle (clone TNT6-1) - human
C;Species: Homo sapiens (man)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995
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A;Accession: A44459
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C;Keywords: alternative splicing; differentiation; skeletal muscle
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A;Title: Two genetically expressed tro
                                                                                                                  A; Reference number: A; Accession: $48793
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R; Farza, H.
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A; Residues: 207-226 < PUT>
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3.2;
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                                           PIDN: CAA56240.1;
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troponin T, skeletal muscle, isoform 4 - chicken
C; Species: Gallus gallus (chicken)
C; Species: Gallus gallus (chicken)
C; Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change
C; Accession: D31957
R; Smillie, L.B.; Golosinska, K.; Reinach, F.C.
J. Biol. Chem. 263, 18816-18820, 1988
A;Title: Sequences of complete cDNAs encoding four variants of cA; Reference number: A92698; MUID:89066672; PMID:3198600
A; Accession: D31957
A; Molecule type: mRNA
A; Residues: 1-251 CSMI>
A; Residues: 1-251 CSMI>
A; Residues: 1-251 CSMI>
troponin T, skeletal muscle, isoform 2 - chicken C; Species: Gallus gallus (chicken) C; Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_charcession: B31957 R; Smillle, L.B.; Golosinska, K.; Reinach, F.C. J. Biol. Chem. 263, 18816-18820, 1988 A; Title: Sequences of complete cDNAs encoding four variants A; Reference number: A92698; MUID:89066672; PMID:3198600 A; Accession: B31957
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        troponin T, fast skeletal muscle, adult alpha (clone 605) - Japanese quall (Species: Coturnix coturnix japonica (Japanese quall) (C:Date: 22-Jun-1990 #sequence_revision 22-Jun-1990 #text_change 13-Aug-1995 C:Accession: B34327 R;Bucher, E.A.; Charles de la Brousse, F.; Emerson Jr., C.P. J. Biol. Chem. 264, 12482-12491, 1989 A;Title: Developmental and muscle-specific regulation of avian fast skeleta A;Reference number: A34327; MUID:89308680; PMID:2745456 A;Accession: B34327
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B31957
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A; Residues: 1-253 <BUC>
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7; Conserv
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7; Conservative
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4; Mismatch
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Pred. No. 8.2;
4; Mismatches
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Pred. No.
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8.2;
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                                                                                                           #text_change 13-Aug-1999
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RESULT
TPRBTS
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A; Molecule type: mRNA
A; Residues: 1-257 <SMI>
A; Cross references: GB:M22155; GB:J04198; NID:g212787; PIDN:AAA49101.1; PID:g212788
C; Superfamily: troponin T
C; Keywords: alternative splicing; muscle; phosphoprotein; skeletal muscle
                                                                                                                                   A; Molecule type: mRNA
A; Residues: 1-263 <SMIN
A; Cross-references: GB:M22156; GB:J04198; NID:g212789; PIDN:AAA49102.1; PID:g212790
C; Superfamily: troponin T
C; Keywords: alternative splicing; muscle; phosphoprotein; skeletal muscle
                                                                                                                                                                                                                                                                                             troponin T, skeletal muscle, isoform 3 - chicken c;Species: Gallus gallus (chicken) C;Date: 31-Mar-1990 *sequence_revision 31-Mar-19 C;Accession: C31957 R;Smillie, L.B.; Golosinska, K.; Reinach, F.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C:Species: Homo sapiens (man)
C:Date: 02-Jul-1996 #text_ct
C:Date: 02-Jul-1996 #text_ct
C:Accession: I53021
R:Wu, Q.L.; Jha, P.K.; Raychowdhury, M.K.; Du, Y.; Leavis,
DNA Cell Biol. 13, 217-233, 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A:Cross-references: GDB:350962; OMIM:600692
A:Map position: 11p15.5-11p15.5
C:Superfamily: troponin T
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A;Status: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: mRNA A;Residues: 1-258 <RES>
В
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A;Tittle: Sequences of complete cDNAs encoding four variants
A;Reference number: A92698; MUID:89066672; PMID:3198600
A;Accession: C31957
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820, 1988
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A; Molecule type: protein
A; Rolecule type: protein
A; Residues: 1-21,39-53 < BR3>
R; Moir, A.J.G.; Cole, H.A.; Perry, S.V.

Biochem. J. 161, 371-382, 1977
A: Title: The phosphorylation sites of troponin T from white skeletal muscle and the effet A: Title: The phosphorylation sites of troponin T from white skeletal muscle and the effet A: Tontents: annotation; phosphorylation sites
A; Contents: annotation; phosphorylation sites
A; Contents: phosphorylation under in vivo conditions occurred at positions that may not be a A: Note: phosphorylation under in vivo conditions occurred at positions that may not be a R: Putney, S.D.; Herlihy, W.C.; Schimmel, P.
Nature 302, 718-721, 1983
A: Title: A new troponin T and cDNA clones for 13 different muscle proteins, found by shd A: Reference number: 146471; MUID:83167564; PMID:6687628
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               troponin T, fast skeletal muscle - rabbit
N;Contains: troponin T, fast skeletal muscle splice form 1; troponin T, fast skeletal muscle splice form 1; troponin T, fast skeletal muscle species: Orycolagus cuniculus (domestic rabbit)
C;Date: 24-Apr-1984 #sequence_revision 17-May-1996 #text_change 22-Jun-1999
C;Accession: A03083; S03590; S03591; S03592; I46515; I46516
R;Pearlstone, J.R; Johnson, P.; Carpenter, M.R.; Smillie, L.B.
J. Biol. Chem. 252, 983-989, 1977
J. Biol. Chem. 252, 983-989, 1977
A;Title: Primary structure of rabbit skeletal muscle troponin-T. Sequence determination A;Reference number: A92220; MUID:77118575; PMID:320204
A;Accession: A03083
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A:Description: binds the troponin complex to tropomyosin; with tropomyosin mediates A:Pathway: muscle contraction C:Superfamily: troponin T: fast skeletal muscle splicing; differentiation; muscle cont C:Keywords: acetylated amino end; alternative splicing; differentiation; muscle cont F:1-266/Product: troponin T: fast skeletal muscle splice form 1 *status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         J. Mol. Biol. 206, 245-249, 1989
A;Title: N-terminal amino acid sequences of three functionally different troponin A;Reference number: $03590; MUID:89199646; PMID:2704041
A;Accession: $03590
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A; Residues: 1-10.17-18, E', 20-48, 50-266 <PE2>
A; Note: this is the final paper in a series
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Residues: 240-266 <PU2>
A;Residues: 240-266 <PU2>
A;Cross-references: EMBL:V00900; NID:g1742; PIDN:CAA24265.1;
C;Complex: troponin is a heterotrimer with one molecule each
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A;Accession: 146516
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A;Molecule type: mRNA
A;Residues: 56-136 <PUT>
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A; Accession: I46515
troponin T, fast skeletal muscle
C; Species: Rattus norvegicus (Nor

                                                                             A24824
                                                                                                            RESULT 15
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A; Accession: S03591
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Keywords: acetylated amino end; alternative splicing; differentiation; muscle contract; 1-266/product: troponin T, fast skeletal muscle splice form 1 *status experimental <w.;1-21.39-266/product: troponin T, fast skeletal muscle splice form 3 *status experiment; 1-10,17-266/product: troponin T, fast skeletal muscle splice form 2 *status experiment; 1-10,17-266/product: troponin T, fast skeletal muscle splice form 2 *status experiment; 1-10,17-266/product: troponin T, fast skeletal muscle splice form 2 *status experiment. //wodified site: acetylated amino end (Ser) *status experimental
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Pred. No. 8.7;
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C;Date: 07-Mar-1988 #sequence_revision 07-Mar-1988 #text_change 23-Feb-1997 C;Accession: A24824 R;Breitbart, R.E.; Nadal-Ginard, B. J. Mol. Biol. 188, 313-324, 1986 J. Mol. Biol. 188, 313-324, 1986 A;Title: Complete nucleotide sequence of the fast skeletal troponin T gene. A;Reference number: A24824; MUID:86281691; PMID:3735424 A;Accession: A24824
В
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                                                                                                                                                   A;Introns: 6/2; 11/1 17/1; 23/1; 28/1; 32/1; 37/1; 43/2; 58/3; 97/3; 123/: C;Superfamily: troponin T
C;Keywords: alternative splicing; muscle; phosphoprotein; skeletal muscle
                                                                                                                                                                                                                            C; Genetics:
                                                                                                                                                                                                                                               A; Molecule type: DNA
A; Residues: 1-272 <BRE>
                                                                                                  Query Match
Best Local (
                                                                                 Matches
103
                                        1 ERAEQQRLKSQ 11
ERAEQQRIRAE 113
                                                                             Similarity 7; Conserv
                                                                                 Conservative
                                                                                                  66.1%;
63.6%;
                                                                                                  Score 41;
Pred. No.
                                                                                 Mismatches
                                                                                                                     DB 2;
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Search completed: March 13, Job time: 13.7636 secs

2003, 18:53:00

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 200000000
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US-08-365-1264-3
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US-08-968-968-97-2
US-08-365-103B-6
US-09-370-612-674-8
US-09-370-612-674-8
US-09-443-184-56
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        Sequence 14, Appl
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Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence
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ALIGNMENTS

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; TOPOLOGY: 11; MOLECULE TYPE: US-08-365-103B-14
                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: Nebel, Heidi S.
REGISTRATION NUMBER: 37,719
REFERENCE/DOCKET NUMBER: Uirf
TELECOMMUNICATION INFORMATION:
TELEPHONE: (515) 288-3667
TELEPAX: (515) 288-1338
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
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                                                                     Query Match
Best Local Similarity
Matches 12; Conserv
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MEDIUM TYPE: Floppy
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Zarley, McKee, Thomte, Voorhees & Sease
STREET: 801 Grand Ave. Suite 3200
CITY: Des Moines
STATE: Iowa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Lynch, Richard G
APPLICANT: Nunez, Raphael D.
APPLICANT: Yodoi, Jungi
TITLE OF INVENTION: DNA Sequences for Soluble Froms of CD23
TITLE OF INVENTION: and Methods of Use for Same
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER:
FILING DATE: 28-DEC-
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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ZIP: 50309
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GENERAL INFORMATION:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                     NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                      TITLE OF INVENTION: DNA Sequences for Soluble Froms of CD23
TITLE OF INVENTION: and Methods of Use for Same
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                      APPLICANT: Lynch, Richard G
APPLICANT: Nunez, Raphael D.
APPLICANT: Yodoi, Jungi
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CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: NODE1, Held1 S.
REGISTRATION NUMBER: 37,719
REFERENCE/DOCKET NUMBER: U1:
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MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                       APPLICANT: Lynch,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: (515) 288-3667
                                                                                              STREET: 801 Grand
CITY: Des Moines
                                                                    COUNTRY: United States
                                                                                                                                                                                                                                                                                                                                                                                               58 RAEQQRLKSQDL 69
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                                                                                                                                       ADDRESSEE
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801 Grand Ave. Suite 3200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            E: Zarley, McKee, Thomte, Voorhees & Scase 801 Grand Ave. Suite 3200
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Nunez, Raphael D.
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100.0%; Pred. No.
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0.015;
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                                                                                         TELEFAX: (515) 288-133
INFORMATION FOR SEQ ID NO:
                                                                                                                      CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Nebel, Held1 S.
REGISTRATION NUMBER: 37,719
REFERENCE/DOCKET NUMBER: U1rf
TELECOMMUNICATION INFORMATION:
TELEPHONE: (515) 288-3667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION: APPLICANT: Lynch,
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                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/365,103B
FILING DATE: 28-DEC-1994
TOPOLOGY: 1: MOLECULE TYPE:
                                                                    SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OPERATING SYSTEM: PC-DO SOFTWARE: Patentin Relaction DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Nunez, Raphael D.
APPLICANT: Yodol, Jungi
TITLE OF INVENTION: DNA Sequences for Soluble Froms of CD23
TITLE OF INVENTION: and Methods of Use for Same
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: protein
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NAME: Nebel, Heldi S.
REGISTRATION NUMBER: 37,719
REFERENCE/DOCKET NUMBER: Uil
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801 Grand Ave. Suite 3200
                                                   321 amino acids
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n Release #1.0, Version #1.25
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Query Match

91.98;

Score 57;

DB 1;

Length 321;

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Query Match
Best Local Similarity
7; Conserve
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                                                  RESULT 6
US-08-961-264-3
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 Sequence 3, Application US/08961264 Patent No. 6025331 GENERAL INFORMATION:
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OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ VEZISO 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/602,941
FILING DATE: 16-FEB-1996
CLASSIFICATION: 514
ATTORNEY/ACENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
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TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                              NAME/KEY: Peptide LOCATION: 1.258 OTHER INFORMATION: OTHER INFORMATION:
                                                                                                                  102 ERAEQQRIRAE 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Poissant, Brian M.
REGISTRATION NUMBER: 28,452
REFERENCE/DOCKET NUMBER: 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: U.S.A. ZIP: 10036-2711
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                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 258 amino acids
TYPE: amino acid
STRANDEDNESS: single
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TELEFAX: 212-869-8864/9741
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                                                                                                                                               1 ERAEQQRLKSQ 11
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Troponin T
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Pred. No. 10;
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US-09-442-099A-3
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Best Local
APPLICANT: Thorn, R.
APPLICANT: Lanser, M.
APPLICANT: Lanser, M.
APPLICANT: Moses, M.
APPLICANT: Wiederschain, D.
TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS COMPRISING TROPONIN SUBUNITS,
TITLE OF INVENTION: FRACMENTS AND HOMOLOGS THEREOF AND METHODS OF THEIR USE TO
TITLE OF INVENTION: INHIBIT ANGIOGENESIS
FILE REFERENCE: 8657-028
CURRENT APPLICATION UNDERSER: US/09/442,099A
CURRENT FILING DATE: 1997-11-17
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TITLE OF INVENTION:
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102 ERAEQQRIRAE 112
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LOCATION:
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                                                                                                                                                                                                                                                                                                         1 ERAEQORLKSQ 11
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10036-2711
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Sequence 3, Application US/09442099A Patent No. 6465431 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/602,94
FILING DATE: 16-FEB-1996
ATTORNEY/AGENT INFORMATION:
NAME: POISSANT, Brian M.
REGISTRATION NUMBER: 28,452
REFERENCE/DOCKET NUMBER: 8657
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212,790-9990
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Langer, Robert S
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COMPRISING TROPONIN SUBUNITS, FRAGMENTS AND ANALOGS
THEREOF AND METHODS OF THEIR USE TO INHIBIT ANGIOGER
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Pred. No. 10;
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; TYPE: PRT
; ORGANISM: Homo saplens
US-09-442-099A-3
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PRIOR FILLING DATE: 1996-02-16
NUMBER OF SEQ ID NOS: 20
SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 3
LENGTH: 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 6, Application US/08961858 Patent No. 5834210
                                                         Matches
                                                                                      Query Match
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                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO: (SEQUENCE CHARACTERISTICS: LENGTH: 288 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: 09/268,274 PRIOR FILING DATE: 1999-03-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Liu, Shigui
APPLICANT: Shi, Qinwei
TITLE OF INVENTION: STABLE TROPONIN SUBUNITS AND COMPLEXES
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber & Jackson
STREET: 411 Hackensack Avenue, 4th Floor
                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: PATENTIA Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/961,858 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                              TOPOLOGY: 15
                                                                                                                                                                                                                                                                  NAME: Jackson Esq., David A.
REGISTATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 1112-1-044 CIP
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
TELEFAX: 201-343-1684
                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
133
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                                                                                                                                                                                                TYPE: a
                                                         Local Similarity tes 7; Conserv
                                                                                                                                                            TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ITY: Hackensack
TATE: New Jersey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: 08/
FILING DATE: 1997-10-30
                           ERAEQQRLKSQ 11
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63.6%;
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                                                          4; Mismatches
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Pred. No.
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Pred. No.
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Mismatches
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; TOPOLOGY: 11r;
; MOLECULE TYPE:
; HYPOTHETICAL: N
US-09-089-593-6
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Best Local Similarity
"---hes 7; Conserve
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US-08-950-925-4
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US-09-089-593-6
                                                                                                                                                                                      Sequence 4, Application US/08950925 Patent No. 6072040
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                                                                                                                        GENERAL INFORMATION:

APPLICANT: Dave, Kirti I.

APPLICANT: Botyanszki, Janos

APPLICANT: Sintar, Eva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEX: 133521
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOCTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                          NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: 201-487-5800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Liu, Shigui
APPLICANT: Shi, Qinwei
TITLE OF INVENTION: STABLE TROPONIN SUBUNITS AND COMPLEXES
                                                                                           TITLE OF INVENTION: Stabilized Conjugates of Uncomplexed TITLE OF INVENTION: Subunits of Multimeric Proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
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TELEFAX: 133521
                                                                                                                                                                                                                                                                                  133 ERAEQQRIRNE 143
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 1112-1-044 CIP
                             ADDRESSEE: MORRISON & FOERSTER STREET: 755 PAGE MILL ROAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/09/089,593 FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: Hackensack
 STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
                                                                                                                                                                                                                                                                                                    1 ERAEQQRLKSQ 11
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5. 6060278
Palo Alto
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Pred. No. 11;
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COMPUTER READABLE FORM:

94304-1018

COUNTRY:

MEDIUM TYPE: Diskette

IBM Compatible

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Query Match
Best Local Similarity
Watches 7; Conservi
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                                                                                                                  ; ORGANISM: Canis familiaris US-09-535-521-20
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                                                                                                                                                         SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 20
LENGTH: 208
                                                                                                                                                                                                                                                                                                                                               Sequence 20, Application US/09535521 Patent No. 6410714 GENERAL INFORMATION:
                                                          Matches
                                                                                   Query Match
                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/09/535,521
CURRENT FILING DATE: 2000-03-24
EARLIER APPLICATION NUMBER: 60/125,913
EARLIER FILING DATE: 1999-03-24
NUMBER OF SEQ ID NOS: 26
                                                                                                                                                                                                                                                                       APPLICANT: Weber, Eric R.
APPLICANT: McCall, Catherine A.
TITLE OF INVENTION: NOVEL CANINE LOW AFFINITY 19E RECEPTOR (CANINE CD23)
TITLE OF INVENTION: PROTEINS, NUCLEIC ACID MOLECULES AND USES THEREOF
FILE REFERENCE: AL-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
ATTORNEY/AGENT INFORMATION:
ATAME: Axford, Laurie A
REGISTRATION NUMBER: 35,053
REFERENCE/DOCKET NUMBER: 3236
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-813-5600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 288 amino acid
                                                                                                                                               TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/950,925
FILING DATE:
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: FRAGMENT TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                   133 ERAEQQRIRNE 143
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TELEFAX: 706141
 16
                                                                       Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 ERAEQORLKSQ 11
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                          2 RAEQQRLKSQD 12
Similarity 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   amino acids
                                                          Conservative
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Pred. No.
                                                                    Score 40; DB
Pred. No. 12;
                                                        Mismatches
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RESULT 12

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APPLICANT: Weber, Eric R.

APPLICANT: McGall, Catherine A.

APPLICANT: MCGall, Catherine A.

TITLE OF INVENTION: NOVEL CANINE LOW AFFINITY IGE RECEPTOR (CANINE CD23)

TITLE OF INVENTION: PROTEINS, NUCLEIC ACID MOLECULES AND USES THEREOF

FILE REFERENCE: AL-5

CURRENT FILING DATE: 2000-03-24

CURRENT APPLICATION NUMBER: 60/125,913

EARLIER APPLICATION NUMBER: 60/125,913

EARLIER APPLICATION NUMBER: 60/125,913

EARLIER FILING DATE: 1999-03-24

NUMBER OF SEQ ID NOS: 26

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 5

LENGTH: 292

TYPE: PRT

ORGANISM: Canis familiaris
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US-08-986-967-2
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LENGTH: 292
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 03...
Thes 7; Conservative
                                                                                                                                                               Patent No. H002023
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                                                                                                                                                                             Sequence
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                GENERAL INFORMATION:

APPLICANT: Hoskins, Jo A.

APPLICANT: Jaskunas Jr., Stanley R.

APPLICANT: Rockey, Pamela K.

APPLICANT: Treadway, Patti J.

TITLE OF INVENTION: Streptococcus Pneumoniae Gene Sequence
TITLE OF INVENTION: GIPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Weber, Eric R.
APPLICANT: WcCall, Catherine A.
APPLICANT: MCCall, Catherine A.
TITLE OF INVENTION: NOVEL CANINE LOW AFFINITY IGE RECEPTOR (CANINE CD23)
TITLE OF INVENTION: PROTEINS, NUCLEIC ACID MOLECULES AND USES THEREOF
FILE REFERENCE: AL-5
CURRENT APPLICATION NUMBER: US/09/535,521
CURRENT FILING DATE: 2000-03-24
EARLIER APPLICATION NUMBER: 60/125,913
EARLIER APPLICATION NUMBER: 60/125,913
EARLIER FILING DATE: 1999-03-24
NUMBER OF SEQ ID NOS: 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: PatentIn Ver. 2.1
NUMBER OF SEQUENCES:
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100 QAEQKRMKAQD 110
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63.6%;
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Pred. No.
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Pred. No.
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Matches
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION UMBER: US/08/986,967
FILING DATE:
CLASSIFICATION: 536
CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                       APPLICANT: Black, Michael
APPLICANT: Hodgson, John
APPLICANT: Knowles, David
APPLICANT: Nicholas, Richard
APPLICANT: Stodola, Robert
TITLE OF INVENTION: No. 6348328el Compounds
NUMBER OF SEQUENCES: 552
CORRESPONDENCE ADDRESS:
ADDRESSE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia
COUNTRY. PA
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Best Local S
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                                                                                                                              COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSED for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/858,207A
FILING DATE: 09-MAY-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/017670
FILING DATE: 14-MAY-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                COUNTRY: USA
ZIP: 19406-0939
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION: TELEPHONE: 317-276-3334
TELEFAX: 317-276-2763
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION: NAME: Webster, Thomas D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
ADDRESSEE: Ell Lilly and Company
STREET: Lilly Corporate Center
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TYPE: amino acid
TOPOLOGY: linear
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CITY: Indianapolis
STATE: Indiana
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REFERENCE/DOCKET NUMBER: X-11756
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Similarity 61.5%;
8; Conservative
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Pred. No.
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Search completed: March 13, 2003, 18:53:53 Job time : 12.5818 secs
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TOPOLOGY: linear
HOLECULE TYPE: NO. 6348328e
US-08-858-207A-293
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Best Local Similarity
Matches 8; Conserv
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SEQUENCE CHARACTERISTICS:
LENGTH: 174 amino acids
TYPE: amino acid
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REFERENCE/DOCKET NUMBER: P5
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-4478
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Pred. No.
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Perfect score:
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Q9J128	Q9J129	Q9J141	Q9J142	09Л152	Q9J163	Q9J176	Q9J194	Q97597	Q9J125	Q9J127	Q9J173	Q9J175	Q9J186	Q9J115	Q9J120	Q9J136	Q9J137	Q9J139	Q9J147	Q9J158	Q9J160	Q9J171	Q9J174	Q9J195	Q9J155	Q9J159	Q9J167	Q9J182
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09j128	Q9j129	095141	29 j 14 2	Q9j152	Q9j163	Q9j176	09j194	097597	Q9j125	09j127	Q9j173	Q9j175	09j186	Q9j115	09j120	Q9j136	Q9j137	Q9j139	Q9j147	Q9j158	29j160	09j171	Q9 j 174	Q9j195	Q9j155	Q9j159	09j167	09j182
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   Q9J181;
Q9J181;
01-OCT-2000
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STRAIN-FIN92168;

Liitsola K., Holmstrom P., Laukkanen T., Brummer-Korvenkonti
Leinikki P., Salminen M.O.;

Leinikki P., Salminen M.O.;

Analysis of HIV-1 genetic subtypes in Finland reveals good

"Analysis of HIV-1 genetic subtypes in Finland reveals good

correlation between molecular and epidemiological data.";

Scand. J. Infect. Dis. 0:0-0(2000).

EMBL; AF219351; AAF30257.1; -.
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Viruses; Retroid viruses; Retroviridae;
NCBI_TaxID=11676;
                                                                                                                                                                                                          Similarity 100
9; Conservative
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(TrEMBLrel. 15, Created)
(TrEMBLrel. 15, Last sequence update)
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Pred. No.
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Analysis of HIV-1 genetic subtypes in correlation between molecular and epide correlation between molecular and epide molecular and epide of the correlation between molecular and epide correlation and epide correlation between molecular and epide correlation and epide cor
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Leinikki P., Salminen M.O.;
"Analysis of HIV-1 genetic subtypes in
correlation between molecular and epide
Scand. J. Infect. Dis. 0:0-0(2000),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NON_TER
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EMBL; AF21933; AAF30239.1; -.
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/iruses; Retrold viruses; Retroviridae; Lentivirus
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Viruses; Retroid viruses; Retroviridae;
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5 KARVLAEAM 13
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9; Conser
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nilarity 100.0%;
Conservative 0
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        PRELIMINARY;
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6077 MW;
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Pred. No.
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Pred. No.
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KARVLAEAM 10

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Best Local Similarity
Matches 9; Conserv
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Best Local
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Q9J144;
Q1-OCT-2000
Q1-OCT-2000
Q1-MAR-2002
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01-OCT-2000
01-OCT-2000
01-MAR-2002
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SEQUENCE
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Leinikki P., Salminen M.O.;
"Analysis of HIV-1 genetic sub
correlation between molecular
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Leinikki P., Salminen M.O.;
"Analysis of HIV-1 genetic subtypes in Finland reveals good correlation between molecular and epidemiological data.";
Scand. J. Infect. Dis. 0:0-0(2000).
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Viruses; Retroid viruses;
VGI_TaxID=11676;
                                                                                        SEQUENCE
                                                                                                                                                 InterPro; IPR001878; Znf_CCHC.
Pfam; PF00098; zf-CCHC; 1.
SMART; SM00343; Znf_C2HC; 1.
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EMBL; AF219329; AAF30235.1; -.
HSSP; P05888; IAAF.
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Viruses; Retroid viruses; Retroviridae;
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56 AA;
                                                                                      58 AA;
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Conservative
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6191 MW;
                                                                                      6414 MW;
                      88.9%;
100.0%;
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Retroviridae;
b; Score 40; DB
b; Pred. No. 1.1
0; Mismatches
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Pred. No.
                                                                                      86B45037A48AE958 CRC64;
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                                           DB 15; Length 58;
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RESULT
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Best Local S
Matches 9
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Best Local Similarity 100.
Matches 9; Conservative
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Q9J138;
01-OCT-2000
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Leinikki P., Salminen M.O.;
"Analysis of HIV-1 genetic subtypes in
correlation between molecular and epide
Scand. J. Infect. Dis. 0:0-0(2000).
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01-OCT-2000 (TrEMBLrel.
01-MAR-2002 (TrEMBLrel.
Gag protein (Fragment).
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Leinikki P., Salminen M.O.;
Leinikki P., Salminen M.O.;
Panalysis of HIV-1 genetic subtypes in Finland reveals good
correlation between molecular and epidemiological data.";
Scand. J. Infect. Dis. 0:0-0(2000).
EMBL: AF719335, AAF302411.; -
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Viruses; Retroid viruses; Retroviridae;
NCBI_TaxID=11676;
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NCBI_TaxID=11676;
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01-MAR-2002
                                                                                                                                                                                                                                                                                                  Pfam; PF00098; zf-CCHC; 1.
SMART; SM00343; ZnF_C2HC; 1.
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SMART; SM00343; ZnF_C2HC; 1.
                                                                                                                                                                                                                   SEQUENCE
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STRAIN-FIN93214;
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09J197;
01-OCT-2000
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01-MAR-2002
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Liitsola K., Holmstrom P., Laukkanen T., Brummer-Korvenkont:
Leinikki P., Salminen M.O.;
"Analysis of HIV-1 genetic subtypes in Finland reveals good
correlation between molecular and epidemiological data.";
Scand. J. Infect. Dis. 0:0-0(2000).
EMBL; AF219305; AAF30211.1; -.
HSSP: P05888; IAAF.
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SMART; SM00343; ZnF_C2HC; 1.
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Viruses; Retroid viruses; Retroviridae;
NCBI_TaxID=11676;
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Leinikki P., Salminen M.O.;
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Viruses; Retroid viruses; Retroviridae; Lentivirus
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88.9%; 5cc.
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                                               EMBL; U70301; AAB09019.1; -. HSSP; P05888; IAAF.
                                                                                                                                                  Human immunodeficiency virus type 1. Viruses; Retroid viruses; Retroviridae; RCBI_TaxID=11676;
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LiltSola K., Holmstrom P., Laukkanen ....

Leinikki P., Salminen M.O.;

Panalysis of HIV-1 genetic subtypes in Finland reveals good

"Analysis of HIV-1 molecular and epidemiological data.";
                                                                                                     STRAIN-RUS9419;
Liitsola K., Laukkanen T., Denisova
Smolskaja T., Ustina V., Vlasov N.,
                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR001878; znf_CCHC. 
Pfam; PF00098; zf-CCHC; 1. 
SMART; SM00343; znf_C2HC; 1.
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                                                                                             Smolskaja T., Ustina V., Vlasov N., "Genetic characterization of HIV-1:
                                                                                                                                 SEQUENCE FROM N.A.
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RESULT 13
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           Liitsola K., Holmstrom P., Laukkanen T

Leinikki P., Salminen M.O.;

"Analysis of HIV-1 genetic subtypes in

correlation between molecular and epid

Scand. J. Infect. Dis. 0:0-0(2000).

EMBL; AF219347; AAF30253.1; -.

HSSP; P05888; 1AAF.

InterPro; IPR001878; Znf_CCHC.

Pfam; PF00098; zf-CCHC; I.

SMARR; SM00343; ZnF_C2HC; 1.
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Scand. J. Infect. Dis. 0:0-0(2000).
EMBL; AF219296; AAF30202.1; -.
HSSP; P05888; 1AAF.
InterPro; IPR001878; Znf_CCHC.
Pfam; PF00098; zf-CCHC; 1.
SMART; SM00347- *~
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Viruses; Retroid viruses; Retroviridae;
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Leinikki P., Salminen M.O.
"Analysis of HIV-1 genetic
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Q9J123;
                    Liitsola K., Holmstrom P., Laukkanen T., Brummer-Korvenkontio H., Leinikki P., Salminen M.O.;
"Analysis of HIV-1 genetic subtypes in Finland reveals good correlation between molecular and epidemiological data.";
Scand. J. Infect. Dis. 0:0-0(2000).
EMBL; AF130284; AAF30190.1; ".
HSSP; P05888; laAF.
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Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID-11676;
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Viruses; Retroid viruses; Retroviridae; Lentivirus
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Leinikki P., Salminen M.O.;
"Analysis of HIV-1 genetic subtypes in F
                                                                                                                                                                                           STRAIN=FIN93230;
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InterPro; IPR001878; Znf_CCHC

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                                 Matches
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                                                                                          Pfam; PF00098; zf-CCHC; 1.
SMART; SM00343; ZnF_C2HC; 1.
                                                                  SEQUENCE
2 KARVLAEAM 10
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2 KARVLAEAM 10
                                 Local Similarity
hes 9; Conserv
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                                 Conservative
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                   88.9%; suc.
y 100.0%; pred. No. _
'''ve 0; Mismatches
                                                                  7117 MW;
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                                                                  FD369389B20186AC CRC64;
                                         DB 15; Length 64;
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Search completed: March Job time: 20.7273 secs 13, 2003, 18:51:57 THIS PAGE BLANK (USPTO)

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Maximum Match 100%
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  GenCore version 5.1.4_p5_4578 (c) 1993 - 2003 Compugen Ltd.
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HSSP; P03351; 1EIA.
HIV; K03457; GAG$RM32.
InterPro; IPR0000721; Gag_p24.
IntexPro; IPR000071; Retrovir_P17.
Pfam; PF00540; Gag_p17; 1.
Pfam; PF005007; Gag_p24; 1.
Zinc-finger.
INIT_MET
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                                                 AIDS; Core protein; Polyprotein; Myristate; Phosphorylation;
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0 131 362 376 >388

BY SIMILARITY.

CORE PROTEIN P17 (MATRIX PROTEIN).

CORE PROTEIN P24 (CORE ANTIGEN).

CORE PROTEIN P2.

CORE PROTEIN P7 (NUCLEOCAPSID PROTEIN).

MYRISTATE (BY SIMILARITY).

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G S	LT 1 HV1W2 GAG_HV1	w ₂	STAN	DARD;		PRT;				
	P05889; 01-NOV-1988 01-FEB-1994	1988	(Rel. (09, Created)		equence :	indate)			
	01-FEB-1994	1994				sequence update)	ipdate)			
200	GAG polyprotein (Fragment). GAG.	yprot ent).	ein [Co	Contains:		Core proteins P17,	ins P17, P24, P2,	P7, P1,	l, P6]	
K () ()	Wiruses	mmuno ; Ret	deficie roid vi	ruses;	Re	<pre>immunodeficiency virus type 1 (ss; Retroid viruses; Retrovirida partn=11705.</pre>	Human immunodeficiency virus type 1 (WMJ2 isolate) (HI Viruses; Retroid viruses; Retroviridae; Lentivirus. NCHT TAYTO.	(HIV-1).		
<i>J</i> 2, 5	[1]		1,00;							
~ ···	MEDLINE-86235450;	E=862354		PubMed=3012778	301	.2778;				
<i>B B</i>	Hahn B. Salahud	B.H., S	Shaw G.M., Taylor M.E., S.Z., Wong-Staal F., Ga	1., Tay	lor	F. Gallo	E., Redfield R.R., Mark Gallo R.C., Parks E.S.	Markham P.D., E.S., Parks W	¥;	•
		C var	lation	in HTL	۱٠.	II/	er time in patients with AIDS or	ts wit	AIDS	유
£	cie	232:	232:1548-1553(1986).	553(198	6					
()()	-!- FUN	FUNCTION:	. PERFORMS)RMS HI	HE	Y COMPLEX	HIGHLY COMPLEX ORCHESTRATED TASKS DURING THE MATURATION, AND INFECTION STAGES OF THE VIRA	KS DUR	ING THE	£ 18
(2()	REF	DICAT	REPLICATION CYCLE. MEMBRANE ASSOCIATION	LE. DU	RIP	W VIRAL A	REPLICATION CYCLE. DURING VIRAL ASSEMBLY, THE PROTEINS FORM MEMBRANE ASSOCIATIONS AND SELF-ASSOCIATIONS THAT ULTIMATELY	EINS FO	ORM ELY	
1212	GAC	SULT I	N BUDDI	ING OF	Ž A	IMMATURE	RESULT IN BUDDING OF AN IMMATURE VIRION FROM THE INFECTED CELL. GAG PRECURSORS ALSO FUNCTION DURING VIRAL ASSEMBLY TO SELECTIVE	10 E	TED CELL. SELECTIVELY	ATS.
	7	THE OND	PACKAC	OWE INO	PLC	DHOSPHORY	BIND AND PACKAGE TWO PLUS STRANDS OF GENOMIC RNA.			
,,,		CELLA	NEOUS:	ISOLAT	ES	MISCELLANEOUS: ISOLATES WMJ1, WMJ2, AND	12, AND WMJ3 WERE OBTAINED FROM	OBTAIN	ED FROM	. <u>«</u>
ດດດ	BLOC WAS	BLOOD SA	SAMPLES SERINATALL	SEQUENT	TEL	DD SAMPLES SEQUENTIALLY TAKEN FROM A PERINATALLY INFECTED BY HER MOTHER.	TWO-YEA	OLD HAI	TIAN WI	8
	This st	d-SSIMS	ROT entr	rv is	3	pyriaht. 1	It is produced thr	ough a	colla	orati
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,,	the Eur	copean	Bioini	Cormati	S	European Bioinformatics Institute.	e. There are no restrictions on	restri	ctions	on its
,,,	use by	non and	-profit	inst	ָּבְּי ק	use by non-profit institutions as long	as	ent is	for on	no way
.,,	entities	s req	requires a	licen	95	agreement (See	(See http://www.isb-sib.ch/announce	isb-sil	b.ch/a	/announce
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                                                                                        EMBL; M62320; AAA75018.1; -.
HSSP; P05888; IAAF.
InterPro; IPR000721; Gag_p24.
InterPro; IPR000071; Retrovir_p17.
InterPro; IPR000078; Znf_CCHC.
Pfam; PF00098; Zf-CCHC; 2.
Pfam; PF00540; Gag_p17; 1.
Pfam; PF00540; Gag_p24; I.
Pfam; PF00540; Gag_p24; I.
Pfam; PF00540; Gag_p34; HIVIMATRIX.
PRINTS; PR00234; HIVIMATRIX.
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                                                                                                                                                                                                                                                                                                                                                                                                                             GAG_HV1U4 STANDARD;
P24736;
01-MAR-1992 (Rel. 21, Created)
ZN_FING
                                                           AIDS; Core p
Zinc-finger;
                                                                         SMART; SM00343; ZnF_C2HC; 2. PROSITE; PS50158; ZF_CCHC; 2
                                                                                                                                                                                                                                                                                                                                Carswell J.W.;
                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
MEDLINE=91090981; PubMcd=2265025;
MEDLINE=91090981; PubMcd=2265025;
                                                                                                                                                                                                                                                                                                                                                                   Viruses; Retroid
NCBI_TaxID=11703;
                                                                                                                                                                                                                                                                                                                                                                                                                01-FEB-1994 (Rel. 28, Last
15-JUN-2002 (Rel. 41, Last
                                                                                                                                                                                                                                                                                                                                                                                  HIV-1).
                                                                                                                                                                                                                                                                                                                                                                                         luman immunodeficiency virus type 1 (strain Ugandan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 KARVLAEAM 10
                                                                                                                                                                                                                                                                                                                                                                                                       FEB-1994 (Rel. 28, Last sequence update)
JUN-2002 (Rel. 41, Last annotation update)
polyprotein (Contains: Core proteins P17, P24, P2,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KARVLAEAM 366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
9; Conserv
                                                                   protein;
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388 AA;
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                                                           Repeat.
                                                                                                                                                                                                                                                                                                                                                                            viruses;
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358
371
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441
492
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43314 MW;
                                                                   Polyprotein;
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      BY SIMILARITY.
CORE PROTEIN P1
CORE PROTEIN P2
CORE PROTEIN P2
CORE PROTEIN P7
CORE PROTEIN P7
CORE PROTEIN P1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0:
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EF885BE10ECF7804 CRC64;
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       PROTEIN P17
PROTEIN P24
PROTEIN P2.
PROTEIN P7 (1
PROTEIN P1.
PROTEIN P1.
PROTEIN P6.
                                                                  Myristate; Phosphorylation;
                                                                                                                                                                                                                                                                                                                                    Clegg J.C.S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                492
                                                                                                                                                                                (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                            Lentivirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 1;
                      (NUCLEOCAPSID PROTEIN)
                                     (CORE ANTIGEN).
                                            (MATRIX PROTEIN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 388
                                                                                                                                                                                                                                                                                                                                      Serwadda D.,
                                                                                                                                                                                                                                                                                                                                                                                          / isolate U455;
                                                                                                                                                                                                      restrictions
                                                                                                                                                                                         and
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                                                                                                                                                                                                              EMBL outstation
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Query Match
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Matches 9
                                                                               HIV: M7323; GAGSNDK.

Interpro; IPR000721; Gag_p24.
Interpro; IPR000771; Retrovir_p17.
Interpro; IPR000071; Retrovir_p17.
Interpro; IPR001078; Znf_CCHC.
Pfam; PF00998; zf-CCHC; 2.
Pfam; PF00540; Gag_p217; 1.
Pfam; PF00540; Gag_p24; 1.
Pfam; PF00607; Gag_p24; 1.
Pfam; PF00607; Gag_p24; 1.
SMART; SM00943; Znf_CCHC; 2.
PROSITE; PS50158; ZF_CCHC; 2.
AIDS; Core Protein; Polyprotein; Myr
Zinc-finger;
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P18800;
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LIPID
SEQUENCE
                                                                                                                                                                                                                                                                                                      EMBL; M27323; AAA44868.1; PIR; JQ0065; FOLJND. HSSP; P05888; 1AAF.
                                                                                                                                                                                                                                                                                                                                                                          entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                           the European Bioinformatics Institute. There use by non-profit institutions as long as modified and this statement is not removed. I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-NOV-1990 (Rel. 16, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
GAG polyprotein (Contains: Core proteins P17,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Spire B., Sire J.,
Hampe A., Chermann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Viruses;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Viruses; Retroid
NCBI_TaxID-11695;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human immunodeficiency virus type 1 (NDK isolate) (HIV-1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-90034200; PubMed-2806917;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nucleotide sequence of HIV1-NDK:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               354 KARVLAEAM 362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -NOV-1990
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MISCELLANEOUS: NDK, ISOLATED FROM A ZAIRIAN PATIENT AIDS, AND IS A HIGHLY CYTOPATHOGENIC STRAIN. SIMILARITY: CONTAINS 2 CCHC-TYPE ZINC FINGERS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FUNCTION: PERFORMS HIGHLY COMPLEX ORCHESTRATED TASKS DURING THE ASSEMBLY. BUDDING, MATURATION, AND INFECTION STAGES OF THE VIRAL REPLICATION CYCLE. DURING VIRAL ASSEMBLY, THE PROTEINS FORM MEMBRANE ASSOCIATIONS AND SELF-ASSOCIATIONS THAT ULTIMATELY RESULT IN BUDDING OF AN IMATURE VIRION FROM THE INFECTED CELL. GAG PRECURSORS ALSO FUNCTION DURING VIRAL ASSEMBLY TO SELECTIVELY BIND AND PACKAGE TWO PLUS STRANDS OF GENOMIC RNA.

THE P24 PROTEIN IS PHOSPHORYLATED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               SWISS-PROT entry is copyright. It is produced through sen the Swiss Institute of Bioinformatics and the EN
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                                                       Repeat.
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J.C.;
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                                                                                    Polyprotein; Myristate;
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BY SIMILARITY.

CORE PROTEIN P17

CORE PROTEIN P24

CORE PROTEIN P2.
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Pred. No.
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MYRISTATE (BY SIMILARITY).
; E4A3B4D633BB6972 CRC64;
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                                                                                        Phosphorylation;
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RESULT 4
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Best Local S
Matches 9
                                                                                  Pfam; PF00098; zf-CCHC; 2.
Pfam; PF00540; Gag_p17; 1.
Pfam; PF00540; Gag_p24; 1.
Pfam; PF00607; Gag_p24; 1.
PRINTS; PR00939; C2HCZNFINGER.
PRINTS; PR00934; HYVIMATELX.
SMART; SM00343; ZnF_C2HC; 2.
PROSITE; PS50158; ZF_CCHC; 2.
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01-FEB-1994 (Rel. 28, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
GAG polyprotein [Contains: Core proteins P17,
                                                                                                                                                                                                                                             EMBL; M26727; AAA83391.1; ...
HSSP; P05888; 1AAF.
HIV; M26727; GAGSOVI.
InterPro; IPR000721; Gag_p24.
InterPro; IPR00071; Retrovir_p17.
InterPro; IPR001878; Znf_CCHC.
                                                                                                                                                                                                                                                                                                                                                                                                   the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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    INIT_MET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Huet T., Dazza M.C., Brun-Vezinet F., Roelants G. A highly defective HIV-1 strain isolated from a individual presenting an atypical western blot.", AIDS 3:707-715(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human immunodeficiency virus type 1 (OYI isolate) (HIV-1).
Viruses; Retroid viruses; Retroviridae; Lentivirus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=90148544; PubMed=2559749;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID-11699;
                                            AIDS; Core protein; Polyprotein; Myristate;
Zinc-finger; Repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 355 KARVLAEAM 363
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FUNCTION: PERFORMS HIGHLY COMPLEX ORCHESTRATED TASKS DURING THE ASSEMBLY, BUDDING, MATURATION, AND INFECTION STAGES OF THE VIRAL REPLICATION CYCLE. DURING VIRAL ASSEMBLY, THE PROTEINS FORM MEMBRANE ASSOCIATIONS AND SELF-ASSOCIATIONS THAT ULTIMATELY RESULT IN BUDDING OF AN IMMATURE VIRION FROM THE INFECTED CELL. GAG PRECURSORS ALSO FUNCTION DURING VIRAL ASSEMBLY TO SELECTIVELY BIND AND PACKAGE TWO PLUS STRANDS OF GENOMIC RNA.

PTM: THE P24 PROTEIN IS PHOSPHORYLATED.

MISCELLANEOUS: THE OXI ISOLATE WAS TAKEN FROM THE BLOOD OF A MISCELLANEOUS: THE VIRION AND PAGE TO THE PAGE THE PAGE TO THE PAGE TO THE PAGE THE PAGE TO THE PA
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Pred. No.
BY SIMILARITY.

CORE PROTEIN P17 (MATRIX PROTEIN).
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                                                                 Phosphorylation;
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PIR; A2553; FOVWH4.

HSSP; P0588; IAAF.

HIV; M13136; GAGSCDC45.

InterPro; IPR000721; Gag_p24.

InterPro; IPR00071; Retrovir_p17.

InterPro; IPR00078; Znf_CCHC.

Pfam; PF00098; Zf-CCHC; 2.

Pfam; PF00098; Zf-CCHC; 2.

Pfam; PF00540; Gag_p17; 1.

PfAm; PF00540; Gag_p24; I.

PFANTS; PR00343; ZNF_CZHC; 2.

SMART; SM00343; ZNF_CZHC; 2.

M00343; ZnF_C2HC; 2. PS50158; ZF_CCHC; 2. re protein; Polyprotein;

Myristate; Phosphorylation;

EMBL; M13136; AAA44306.1;

or send an email to license@isb-sib.ch).

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           T Molecular cloning and primary nucleotide sequence analysis of a red distinct human immunodeficiency virus isolate reveal significant red divergence in its genomic sequences. "; Proc. Natl. Acad. Sci. U.S.A. 83:8380-8384(1986).

11. Proc. Natl. Acad. Sci. U.S.A. 83:8380-8384(1986).

12. C. ASSEMBLY, BUDDING, MATURATION, AND INECTION STAGES OF THE VIRAL RESEMBLY, BUDDING, MATURATION, AND INECTION STAGES OF THE VIRAL RESEMBLY. THE PROTEINS FORM MEMBRANE ASSOCIATIONS AND SELF-ASSOCIATIONS THAT ULTIMATELY RESULT IN BUDDING OF AN IMMATURE VIRION FROM THE INFECTED CELL.

12. C. GAG PRECURSORS ALSO FUNCTION DURING VIRAL ASSEMBLY TO SELECTIVELY OF THE P24 PROTEIN IS PHOSPHORYLATED.

13. C. -!- SIMILARITY: CONTAINS 2 CCHC-TYPE ZINC FINGERS.
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P05887;
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01-FEB-1994 (Rel. 28, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
GAG polyprotein (Contains: Core proteins P17,
                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
MEDLINE-87041461: PubMed-3490666;
Desai S.M., Kalyanaraman V.S., Casey J.M., Srinivasan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Andersen P.R., Devare S.G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID-11687;
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(BY SIMILARITY).
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1.4;
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RESULT 6
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Best Local
Pfam; PF00098; Z. CONTROL Pfam; PF00540; Gag_p24; 1. Pfam; PF00607; Gag_p24; 1. Pfam; PF00607; PR00939; CZHCZNFINGER. PRINTS; PR00234; HIVIMATRIX. SMART; SM00343; ZnF_C2HC; 2. SMART; SM00343; ZnF_CCHC; 2.
                                                                                                                                                                                                                                   EMBL; K03454;
EMBL; A07108;
HSSP; P05888;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13-AUG-1987
01-FEB-1994
15-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Alizon M., Wain-Hobson S., Montagnier L.,
"Genetic variability of the AIDS virus: no
of two isolates from African patients.";
Cell 46:63-74(1986)
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                                                                                                                                           HIV; K03454; GAGSELI.
InterPro; IPR000721; Gag_p24.
InterPro; IPR000071; Retrovir_p17.
InterPro; IPR001878; Znf_CCHC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human immunodeficiency virus type 1 (ELI isolate) (HIV-1).
Viruses; Retroid viruses; Retroviridae; Lentivirus.
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INIT_MET
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(Rel. 28, Last sequence update)
(Rel. 41, Last annotation update)
(tein [Contains: Core proteins P17, P24, P2, P7,
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Pred. No.
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023CA76C9C6F22AD CRC64;
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E PROTEIN P1.
E PROTEIN P6.
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RESULT 7
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Best Local :
Pfam; PF000540; Gag_D17; 1.
Pfam; PF000540; Gag_D24; 1.
Pfam; PF000607; Gag_D24; 1.
PRINTS; PR00939; C2HCZNFIKGER.
PRINTS; PR00234; HIV1MATRIX.
PRINTS; PR00234; ZnF_C2HC; 2.
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Zinc-finger;
INIT_MET
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01-FEB-1994
15-JUN-2002
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P04591;
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                                                               HIV; K03455; GAGSHXB2.
Interpro; IPR0007721; Ggs_p24.
Interpro; IPR000071; Retrovir_p17.
Interpro; IPR001878; Znf_CCHC.
pfam; PF00098; Zf-CCHC; 2.
                                                                                                                               EMBL;
                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a content the Every series institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and fo entitles requires a license agreement (See http://www.isb-sib.
                                                                                                                                                                                                                                                                                                                                                                                     AIDS
                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-87299196; PubMed-3040055;
Ratner L., Fisher A., Jagodzinski L.L., Mitsuya H.,
Gallo R.C., Wong-Staal F.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15-JUN-2002 (Rel. 41, Last annotation update) GAG polyprotein (Contains: Core proteins P17,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CHAIN
                                                                                                                                                                    or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Viruses; Retroid viruses;
NCBI_TaxID=11706;
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Viruses; Retroid viruses; Retroviridae; Lentivirus.
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SIMILARITY: CONTAINS 2 CCHC-TYPE ZINC FINGERS.
                                                                                                                                                                                                                                                                               S Res. Hum. Retroviruses 3:57-69(1987).

S Res. Hum. Retroviruses 3:57-69(1987).

FUNCTION: PERFORMS HIGHLY COMPLEX ORCHESTRATED TASKS DURING THE ASSEMBLY, BUDDING, MATURATION, AND INFECTION STAGES OF THE VIRAL REPLICATION CYCLE. DURING VIRAL ASSEMBLY, THE PROTEINS FORM MEMBRANE ASSOCIATIONS AND SELF-ASSOCIATIONS THAT ULTIMATELY RESULT IN BUDDING OF AN IMMATURE VIRION FROM THE INFECTED CELL. GAG PRECURSORS ALSO FUNCTION DURING VIRAL ASSEMBLY TO SELECTIVELY BIND AND PACKAGE TWO PLUS STRANDS OF GENOMIC RNA.

PTM: THE P24 PROTEIN IS PHOSPHORYLATED.
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                                                                                                                             P05888; 1AAF
                                                                                                                                         K03455; AAB50258.1;
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(Rel. 28, Last sequence update)
(Rel. 41, Last annotation update)
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MYRISTATE (BY
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Pred. No.
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                                                                                                                                                                                                                                   a collaboration -
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RESULT 8
GAG_HV1J3
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                                                                      EMBL; M21137; AAB03522.1; -.
HSSP; P0588; IAAF.
HIV; M21137; GASSJH3.
InterPro; IPR000721; Gag_p24.
InterPro; IPR000771; Retrovir_p17.
InterPro; IPR001878; Daf_CCHC.
Pfam; PF00098; zf-CCHC; 2.
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ZN_FING
LIPID
Pfam; PF00540; Gag_p17; 1.
Pfam; PF00540; Gag_p24; 1.
Pfam; PF00607; Gag_p24; 1.
PRINTS; PR00939; C2HCZNFINGER.
PRINTS; PR00234; HIVIMATRIX.
PRINTS; PR00234; ZnF_C2HC; 2.
                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                    KOMIYAMA N., HATTOTI N., INDUE J., SAKUMA S., KURIMURA T., YOShida M., "NUCLEOTIDE SEQUENCES OF 939 and env genes of a Japanese isolate of HIV-1 and their expression in bacteria.";
AIDS Res. Hum. Retroviruses 5:411-419(1989).
-1- FUNCTION: PERFORMS HIGHLY COMPLEX ORCHESTRATED TASKS DURING THE ASSEMBLY, BUDDING, MATURAPTION, AND INFECTION STACES OF THE VIRAL REPLICATION CYCLE. DURING VIRAL ASSEMBLY, THE PROTEINS FORM MEMBRANE ASSOCIATIONS AND SELF-ASSOCIATIONS THAT ULTIMATELY RESULT IN BUDDING OF AN IMMATURE VIRION FROM THE INFECTED CELL. GAGG PRECURSORS ALSO FUNCTION DURING VIRAL ASSEMBLY TO SELECTIVELY BIND AND PACKAGE TWO PLUS STRANDS OF GENOMIC RNA.
-1- PTM: THE P24 PROTEIN IS PHOSPHORYLATED.
-1- SIMILARITY: CONTAINS 2 CCHC-TYPE ZINC FINGERS.
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01-FEB-1994 (Rel. 28, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
GAG polyprotein (Contains: Core proteins P17,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Zinc-finger;
INIT_MET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human immunodeficiency virus type 1 (JH3 isolate) (HIV-1).
Viruses; Retroid viruses; Retroviridae; Lentivirus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=89352108; PubMed=2669897;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=11694;
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9; Conser
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CORE PROTEIN P24 (CORE ANTIC CORE PROTEIN P2.

CORE PROTEIN P7 (NUCLEOCAPSICORE PROTEIN P1.

CORE PROTEIN P1.

CORE PROTEIN P6.

CORE PROTEIN P6.

CCHC-TYPE 1.

CCHC-TYPE 2.

MYRISTATE (BY SIMILARITY).

MYRISTATE (BY SIMILARITY).
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Pred. No.
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RESULT 9
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Best Local
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Q70622;
15-JUL-1998
15-JUL-1998
15-JUN-2002
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ZN_FING
LIPID
                                                                                                                                                                                                                                                                                                                        Reitz M.S. Jr., Hall L., Robert-Guroff M., Lautenberger J., Hahn B.M., Shaw G.M., Kong L.I., Welss S.H., Waters D., Gallo R.C., Blattner W.; "Viral variability and serum antibody response in a laboratory worker infected with HIV type 1 (HTLV type IIB)."; AIDS Res. Hum. Retroviruses 10:1143-1155(1994).

AIDS Res. Hum. Retroviruses 10:1143-1155(1994).

-i- FUNCTION: PERFORMS HIGHLY COMPLEX ORCHESTRATED TASKS DURING THE ASSEMBLY, BUDDING, MATURATION, AND INFECTION STACES OF THE VIRAL REPLICATION CYCLE. DURING VIRAL ASSEMBLY, THE PROTEINS FORM MEMBRANE ASSOCIATIONS AND SELE-ASSOCIATIONS THAT ULTIMATELY RESULT IN BUDDING OF AN INMATURE VIRION FROM THE INFECTED CELL. GAG PRECURSORS ALSO FUNCTION DURING VIRAL ASSEMBLY TO SELECTIVELY BUDDING OF AN INMATURE VIRION FROM THE INFECTED CELL.
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PRINTS; PRO0939; C2HCZNFINGE
PRINTS; PRO0234; HIVIMATRIX.
                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                          Pfam; PF00098; zf-CCHC; 2.
Pfam; PF00540; Gag_p17; 1.
Pfam; PF00607; Gag_p24; 1.
PRINTS; PR00939; C2HCZNFINGER.
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                                                                                 InterPro; IPR000721; Gag_p24.
InterPro; IPR000071; Retrovir_p17.
InterPro; IPR001878; Znf_CCHC.
                                                                                                                             EMBL; U12055; AAA76686.1;
HSSP; P05888; 1AAF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Viruses;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=95127297;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=82834;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human immunodeficiency virus type 1 (LW12.3 isolate) (HIV-1).
Viruses; Retroid viruses; Retroviridae; Lentivirus.
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JUL-1998 (Rel. 36, Last seque
JUN-2002 (Rel. 41, Last annot
polyprotein [Contains: Core
                                                                                                                                                                                                                                                                                 BIND AND PACKAGE TWO PLUS STRANDS OF GENOMIC RNA. PTM: THE P24 PROTEIN IS PHOSPHORYLATED. SIMILARITY: CONTAINS 2 CCHC-TYPE ZINC FINGERS.
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annotation update)
Core proteins P17,
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CORE PROTEIN P
CORE PROTEIN P
CORE PROTEIN F
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Pred. No.
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MYRISTATE (BY SIMILARITY).
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Best Local
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                                                      Pfam; PF00098; Zf-CCHC; Z.
Pfam; PF00540; Gag_p17; 1.
Pfam; PF00540; Gag_p24; 1.
Pfan; PF00607; Gag_p24; 1.
PR.NTS; PR00939; C2HCZNFINGER.
PR.NTS; PR00234; HIVLMATRIX.
SMART; SM00343; ZnF_C2HC; 2.
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P12493;
01-OCT-1989
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CHAIN
Zinc-finger;
                  SMART; SM00343; ZnF_C2HC; 2.
PROSITE; PS50158; ZF_CCHC; 2.
AIDS; Core protein; Polyprotein;
                                                                                                                                                                             InterPro; IPRO00721; Gag_p24.
InterPro; IPRO00071; Retrovir_p17.
InterPro; IPRO01878; Znf_CCHC.
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                                                                                                                                                                                                                                                                                                                        use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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15-JUN-2002 (Rel. 41, Last annotation update)
GAG polyprotein (Contains: Core proteins P17, P24, P2, P7, P1, P6).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /iruses;
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(Rel. 28, Last seq.
(Rel. 41, Last ann
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ciency virus type 1 (New York-5 isolate) (HIV-1).
viruses; Retroviridae; Lentivirus.
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MYRISTATE (BY SIMILARITY).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 40;
Pred. No.
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                  Myristate; Phosphorylation;
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E PROTEIN P2.
E PROTEIN P7 (
E PROTEIN P1.
E PROTEIN P6.
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There are no restrictions
ong as its content is in
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ZN_FING
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P35962;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CHAIN
                                                                                                                                                                entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a between the Swiss Institute of Bioinformatics and the EMBI the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and institutions as the statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CHAIN
                                                                                                              PIR; A44001; A44001.
HSSP; P0588B; lAAF.
                                                                                                                                        EMBL; M93258; -; NOT_ANNOTATED_CDS
                                                                                                                                                                                                                                                                                                                                                           J. Virol. 66:6587-6600(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                       Shaw G.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human immunodeficiency virus type 1 (YU-2 isolate) (HIV-1). Viruses; Retroid viruses; Retroviridae; Lentivirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GAG polyprotein
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                                                                                                                                                                                                                                                                                                                                                                                              properties of human immunodeficiency virus type 1
                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. MEDLINE=93021387; PubMed=1404605;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=36377;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                          'Complete nucleotide sequence, genome organization,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      358 KARVLAEAM 366
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                                                                                                                                                                                                                                                                SIMILARITY: CONTAINS 2 CCHC-TYPE ZINC FINGERS.
                                                                                                                                                                                                                                                                          ASSEMBLY, BUDDING, MATURATION, AND INFECTION STAGES OF THE VIRAL REPLICATION CYCLE. DURING VIRAL ASSEMBLY, THE PROTEINS FORM MEMBRANE ASSOCIATIONS AND SELF-ASSOCIATIONS THAT ULTIMATELY RESULT IN BUDDING OF AN IMMATURE VIRION FROM THE INFECTED CELL. GAG PRECURSORS ALSO FUNCTION DURING VIRAL ASSEMBLY TO SELECTIVELY BIND AND PACKAGE TWO PLUS STRANDS OF GENOMIC RNA. PTM: THE P24 PROTEIN IS PHOSPHORYLATED.
                                                                                                                                                                                                                                                                                                                                                                                   limited defectiveness and complementation.";
                                                                                                                                                                                                                                                                                                                                                                                                                                 Hui H., Burgess C.J., Price R.W., Sharp P.M., Hahn B.H.,
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9; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (Rel. 29, Created)
(Rel. 29, Last sequence update)
(Rel. 41, Last annotation update)
tein [Contains: Core proteins P17,
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CORE PROTEIN P
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Pred. No.
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MYRISTATE (BY SIMILARITY)
C8ECC1302FE2C1E2 CRC64;
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                                                                                                                                                                             (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 1;
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Interpro; IPR000721; Gag_p24.
Interpro; IPR00071; Retrovir.p17.
Interpro; IPR000871; Retrovir.p17.
Interpro; IPR001878; Znf_CCHC.
Pfam; PF00098; Zf-CCHC; 2.
Pfam; PF00540; Gag_p217; 1.
Pfam; PF00607; Gag_p24; 1.
PRINTS; PR00939; C2HCZNFINGER.
PRINTS; PR00934; HIVIMATRIX.
SMART; SW00343; ZnF_CJHC; 2.
PROSITE; PS50158; ZF_CCHC; 2.

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RESULT 12
GAG_HV1Z2
ID GAG_HV1Z2
AC P12495;
DT 01-FEB-1985
DT 01-F
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Best Local
                                                                                    Pfam; PF00098; zf-CCHC; 2.
Pfam; PF00540; Gag_P17; 1.
Pfam; PF00507; Gag_P24; 1.
PRINTS; PR00939; C2HCZNFINGER.
PRINTS; PR00234; HIVIMATRIX.
SMART; SM00343; ZnF_CZHC; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LIPID
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (NOV-1988) to the HIV data bank.

-i- FUNCTION: PERFORMS HIGHLY COMPLEX ORCHESTRATED TASKS DURING THE ASSEMBLY, BUDDING, MATURATION, AND INFECTION STAGES OF THE VIRA REPLICATION CYCLE. DURING VIRAL ASSEMBLY, THE PROTEINS FORM MEMBRANE ASSOCIATIONS AND SELF-ASSOCIATIONS THAT ULTIMATELY RESULT IN BUDDING OF AN IMMATURE VIRION FROM THE INFECTED CELL.
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                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                            HSSP; P05888; IAAF.
HIV; M22639; GAGS2226.
InterPro; IPR000721; Gag_p24.
InterPro; IPR000071; Retrovir_p17.
InterPro; IPR001878; Znf_CCHC.
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15-JUN-2002
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01-OCT-1989
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Viruses; Retroid viruses; Retroviridae; Lentivirus.
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INIT_MET
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                       AIDS; Core protein; Polyprotein; Myristate; Phosphorylation; Zinc-finger; Repeat.
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                                                                        PROSITE; PS50158; ZF_CCHC;
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                                                                                                                                                                                                                                                                                                                                             M22639; AAA45365.1;
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. 41, Last anno
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Core proteins P17,
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CORE PROTEIN P2.4 (CO
CORE PROTEIN P2.
CORE PROTEIN P7 (NUC
CORE PROTEIN P1.
CORE PROTEIN P6.
CCHC-TYPE 1.
CCHC-TYPE 2.
MYRISTATE (BY SIMILA
MY: 278E665F5405CD99 (MJ
CORE PROTEIN P6.
CCHC-TYPE 2.
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Pred. No.
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1.4;
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InterPro; LPROUVE, 2.
pfam; pF00098; zf-CCHC; 2.
pfam; pF00540; Gag_pl7; 1.
pfam; pF00607; Gag_p24; 1.
pfam; pF00607; Gag_p24; 1.
pRINTS; pR00939; CZHCZNFIKGER.
PRINTS; pR00934; HIVIMATRIX.
SMART; SM00343; ZDF_CCHC; 2.

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RESULT 13
GAG_HV1A2
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                                                                              HSSP; P05888; IAAF.
HIV; K02007; GAGSSF2.
InterPro; IPR000721; Gag_p24.
InterPro; IPR000071; Retrovir_p17.
InterPro; IPR001878; Znf_CCHC.
                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-FEB-1994 (Rel. 28, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
GAG polyprotein [Contains: Core proteins P17,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21-JUL-1986 (Rel. 01,
01-FEB-1994 (Rel. 28,
15-JUN-2002 (Rel. 41,
                                                                                                                                                                                                                                                                                                                                                                                        (ARV-2).";
Science 227:484-492(1985).
-!- FUNCTION: PERFORMS HIG
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                                                                                                                                   PIR; A03947; FOVWA2. HSSP; P05888; 1AAF.
                                                                                                                                                          EMBL; K02007; AAB59875.1;
                                                                                                                                                                                                                                                                                                                                                                                                                            "Nucleotide sequence and expression of an AIDS-associated retrovirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID-11685;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human immunodeficiency virus type 1 (ARV2/SF2 isolate) (HIV-1).
Viruses; Retroid viruses; Retroviridae; Lentivirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 P03349;
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                                                                                                                                                                                                                                                                                  FUNCTION: PERFORMS HIGHLY COMPLEX ORCHESTRATED TASKS DURING THE ASSEMBLY, BUDDING, MATURATION, AND INFECTION STRACES OF THE VIRAL REPLICATION CYCLE. DURING VIRAL ASSEMBLY, THE PROTEINS FORM MEMBRANE ASSOCIATIONS AND SELF-ASSOCIATIONS THAT ULTIMATELY RESULT IN BUDDING OF AN IMMATURE VIRION FROM THE INFECTED CELL. GAG PRECURSORS ALSO FUNCTION DURING VIRAL ASSEMBLY TO SELECTIVEL BIND AND PACKAGE TWO PLUS STRANDS OF GENOMIC RNA. PM: THE P24 PROTEIN IS PHOSPHORVLATED.
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0; Mismatches
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P7 (NUCLEOCAPSID PROTEIN).
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RESULT 14

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GAG_H

AC P2087

AC P2087

DT 01-FE

DT 01-FE

DT 01-FE

DT 02-FE

CG GAG

CC I-F

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Best Local S
Matches 9
                                                                     EMBL; M38429; AAB03744.1; -.
HSSP; P0588; IAAF.
HIV; M38429; GAG$JRCSF.
IntcrPro; IPR000721; Gag_p24.
IntcrPro; IPR00071; Retrovir_p17.
IntcrPro; IPR00078; Znf_CCHC.
Pfam; PF00098; Zf-CCHC; 2.
Pfam; PF00540; Gag_p17; 1.
Pfam; PF00540; Gag_p17; 1.
Pfam; PF00607; Gag_p24; 1.
PRNTS; PR00234; HIVIMATRIX.
SMART; SM00343; ZnF_CCHC; 2.
PROSITE; PS50158; ZF_CCHC; 2.
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P20873;
01-FEB-1991 (Rel. 17, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
GAG polyprotein [Contains: Core proteins P17, P24, P2, P7, P1,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZN_FING
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                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Koyanagi S., Chen I. Submitted (DEC-1988)
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Viruses; Retroid viruses; Retroviridae; Lentivirus.
AIDS; Core protein;
Zinc-finger; Repeat
INIT_MET 0
                                                                                                                                                                                                                                                                                                                                                                                                             or send an email to license@isb-sib.ch).
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Zinc-finger; Repeat
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mitted (DEC-1998) to the HIV data bank.

function: performs Highly Complex orchestrated tasks during the function. Performs Highly Complex orchestrated tasks during the restance of the Viral ASSEMBLY, BUDDING, MATURATION, AND INFECTION STAGES OF THE VIRAL REPLICATION CYCLE. DURING VIRAL ASSEMBLY, THE PROTEINS FORM MEMBRANE ASSOCIATIONS AND SELF-ASSOCIATIONS THAT ULTIMATELY MEMBRANE ASSOCIATIONS AND SELF-ASSOCIATION THE INFECTED CELL. GAG PRECURSORS ALSO FUNCTION DURING VIRAL ASSEMBLY TO SELECTIVELY BIND AND PACKAGE TWO PLUS STRANDS OF GENOMIC RNA.

PTM: THE P24 PROTEIN IS PHOSPHORYLATED.

SIMILARITY: CONTAINS 2 CCHC-TYPE ZINC FINGERS.
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ORE PROTEIN P17

ORE PROTEIN P24

ORE PROTEIN P2.

ORE PROTEIN P1.
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                   EMBL; X04415; CAA28011.1; -.
EMBL; A07116; CAA00618.1; -.
HSSP; POS5888; IAAF.
HIV: K03456; GAG$MAL.
InterPro; IPR000721; Gag_p24.
InterPro; IPR00071; Retrovir_p17.
InterPro; IPR001878; Znf_CCHC.
Pfam; PF00098; zf-CCHC; 2.
Pfam; PF00540; Gag_p17; 1.
Pfam; PF00540; Gag_p24; 1.
PRNTS; PR00234; HIVIMATRIX.
SMART; SM00343; ZNF_CCHC; 2.
PROSITE; PS50188; ZF_CCHC; 2.
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13-AUG-1987 (Rel. 05, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
GAG polyprotein [Contains: Core proteins P17,
                                                                                                                                                                                                                                                                                                                                                                                                                           Alizon M., Wain-Hobson S., Montagnier L., "Genetic variability of the AIDS virus: nu of two isolates from African patients."; Cell 46:63-74(1986).
                                                                                                                                                                                                                                    use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                         This
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                                                                                                                                                                                                                        entities requires a license agreement (See http://www.isb-sib.ch/announce/
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NCBI_TaxID=11697;
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                                                                                                                                                                                                                                                                                                            FUNCTION: PERFORMS HIGHLY COMPLEX ORCHESTRATED TASKS DURING THE ASSEMBLY, BUDDING, MATURATION, AND INTECTION STAGES OF THE VIRAL REPLICATION CYCLE. DURING VIRAL ASSEMBLY, THE PROTEINS FORM MEMBRANE ASSOCIATIONS AND SELF-ASSOCIATIONS THAT ULTIMATELY RESULT IN BUDDING OF AN IMMATURE VIRION FROM THE INFECTED CELL. GAG PRECURSORS ALSO FUNCTION DURING VIRAL ASSEMBLY TO SELECTIVELY BIND AND PACKAGE TWO PLUS STRANDS OF GENOMIC RNA. PTM: THE P24 PROTEIN IS PHOSPHORYLATED.
                                                                                                                                                                                                                                                                          SWISS-PROT entry is copyright. It is produced through a 
een the Swiss Institute of Bioinformatics and the EMBI
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CORE PROTEIN P6.

CCHC-TYPE 1.

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FT CHAIN 138 368 CORE PROTEIN P24 (CORE ANTIGEN).
FT CHAIN 369 383 CORE PROTEIN P2.
FT CHAIN 384 437 CORE PROTEIN P2.
FT CHAIN 454 504 CORE PROTEIN P1.
FT CHAIN 454 504 CORE PROTEIN P1.
FT ZN_FING 395 412 CCHC_TYPE 1.
FT ZN_FING 416 433 CCHC_TYPE 2.
FT LIPID 1 1 MYRISTATE (BY SIMILARITY).
SQ SEQUENCE 504 AA; 56001 MW; 7F96785683D398B3 CRC64;
Query Match 88.9%; Score 40; DB 1; Length 504;
Best Local Similarity 100.0%; Pred. No. 1.4;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 KARVLAEAM 10 | HIIIIII | Db 364 KARVLAEAM 372

Search completed: March 13, 2003, 18:49:54

Job time: 6.27273 secs
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A;Residues: 1-75 <SAL>
A;Cross-references: EMBL:211148; NID:960078; PIDN:CAA77499.1;
C;Superfamily: AIDS-related virus gag polyprotein
C;Keywords: polyprotein
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A;Cross-references: EMBL:Z11142; NID:g60101; PIDN:CAA77493.1; PID:g60102 C;Superfamily: AIDS-related virus gag polyprotein C;Keywords: polyprotein
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                                                                                                                2 KARVLAEAM 10
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KARVLAEAM 10
                                                                                                                                                                                                                                Similarity
9; Conserv
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                                                                                                                                                                                                                                                                                              100.0%;
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100.0%; Pred. No.
tive 0; Mismatch
                                                                                                                                                                                                                                                                                                                                                      88.9%;
                                                                                                                                                                                                                                      0
                                                                                                                                                                                                                                                                                              Score 40; pred. No.
                                                                                                                                                                                                                                      Mismatches
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0.5;
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gag polyprotein - human immunodeficiency virus type 1 (isolate IV)
N;Alternate names: assemblin; core polyprotein; gag precursor
N;Contains: capsid antigen core protein p24CA; core protein p1; core protein p6; matrix
C;Species: human immunodeficiency virus type 1, HIV-1
C;Date: 17-May-1985 #sequence_revision 17-May-1985 #text_change 05-Dec-1998
C;Accession: A03948
R;Muesing, M.A.; Smith, D.H.; Cabradilla, C.D.; Benton, C.V.; Lasky, L.A.; Capon, D.J.
Nature 313, 450-458, 1985
A;Title: Nucleic acid structure and expression of the human AIDS/lymphadenopathy retrov
A;Reference number: A93355; MUID:85111157; PMID:2982104
A;Accession: A03948
A;Residues: 1-478 <AUE>
C;Genetics:
A;Genetics:
A;Genetics: ADS; blocked amino end; core protein; immunodeficiency; lipoprotein; myris
F;2-478/Product: gag precursor (assemblin) #status predicted <P17>
F;2-132/Product: matrix antigen core protein p17MA #status predicted <P17>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      polyprotein - human immunodeficiency virus type 1
C;Specles; human immunodeficiency virus type 1, HIV-1
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 2
C;Accession: S24476; S24489
R;Salminen, M.
submitted to the EMBL Data Library, October 1991
A;Reference number: S24471
A;Reference number: S24471
A;Accession: S24476
A;Status: preliminary
A;Molecule type: DNA
A;Residues; 1-76 <SALD
A;Cross-references: EMBL:Z11143; NID:g60103; PIDN:CAA77494.1; PID
C;Superfamily: AIDS-related virus gag polyprotein
C;Keywords: polyprotein
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C;Species: human immunodeficiency virus type 1, HTV-1
C;Date: 20-Feb-195 #sequence_revision 20-Feb-1995 #text_change 26-Aug-1999
C;Accession: $24474; $24487
R;Salminen, M.
submitted to the EMBL Data Library, October 1991
A;Reference number: $24471
A;Reference number: $24471
A;Accession: $24474
A;Accession: $24474
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-75 <SAL>
A;Cross-references: EMBL:Z11138; NID:g60095; PIDN:CAA77489.1; PID:g60096
C;Superfamily: AIDS-related virus gag polyprotein
C;Keywords: polyprotein
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Best Local (
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2 KARVLAEAM 10
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9; Conserv
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9; Conserv
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Query Match

Score 40;

DB 2;

Length 498;

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A;Note: host Homo sapiens (man)
C;Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 16-Jul-1999
C;Accession: J00065
R;Spire, B.; Sire, J.; Zachar, V.; Rey, F.; Barre-Sinoussi, F.; Galibert, F.; Gene 81, 275-284, 1989
A;Title: Nucleotide sequence of HIV1-NDK: a highly cytopathic strain of the hu A;Reference number: J00065; MUID:90034200; PMID:2806917
                                                                                                                                                                                                     gag polyprotein - human immunodeficiency virus type 1 (strain JRFL) C;Species: human immunodeficiency virus type 1, HIV-1 C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 24-C;Accession: T09436 R;Pang, S.; Vinters, H.V.; Akashi, T.; O'Brien, W.A.; Chen, I.S.; K submitted to the EMBL Data Library, July 1996
                                                                                                                                                                                                                                                                                                                                               RESULT
T09436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Superfamily: AIDS-related virus gag polyprotein C;Keywords: AIDS; core protein; immunodeficiency; polyprotein F;1-129/Product: core protein p17 #status predicted <C17> F;130-389/Product: core protein p24 #status predicted <C24> F;390-497/Product: core protein p15 #status predicted <C15>
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F;413-426/Region: zinc finger CCHC motif
F;247Modified site: myristylated amino end (Gly) (in mature form) #status predicted
F;392,395,400,405/Binding site: zinc (Cys, Cys, His, Cys) #status experimental
F;413,416,421,426/Binding site: zinc (Cys, Cys, His, Cys) #status experimental
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F;110-114/Region: nuclear location signal
F;110-114/Region: nuclear location signal
F;133-363/Product: capsid antigen core protein p24CA #status predicted <P24>
F;33-3-37/Product: core protein p2 #status predicted <CP2>
F;378-432/Product: nucleocapsid core protein p7NC #status predicted <CP7>
  A;Gene: gag
C;Superfamily:
                                                                                            A; Molecule type: DNA
A; Residues: 1-498 <P
                                                                                                                                                          A; Reference number: Z16673
A; Accession: T09436
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                                               C; Genetics:
                                                                                                                                     A; Status: preliminary; translated from GB/EMBL/DDBJ
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A; Residues: 1-497
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                                                                    A; Cross-references:
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9; Conserv
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9; Conserv
    AIDS-related virus
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                                                                    EMBL: U63632;
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100.0%; Pr/
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100.0%; Pr
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Pred. No.
                                                                    NID:g1465777; PID:g1465778
gag
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Pred. No
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C;Accession: A44001

R; Hui, Y; Hui, H; Burgess, C.J.; Price, R.W.; Sharp, P.M.; Hahn, B.H.; Shaw, G.M.
J. Virol. 66, 6587-6600, 1992

A;Title: Complete nucleotide sequence, genome organization, and biological properties A;Reference number: A44001; MUID:93021387; PMID:1404605

A;Accession: A44001

A;Coession: A44001

A;Cross-references: GB:M93258
C;Genetics: 1-500 <LIY>
A;Cross-references: GB:M93258
C;Genetics: A;Gene: gag
C;Superfamily: AIDS-related virus gag polyprotein
C;Keywords: AIDS; core protein; immunodeficiency; polyprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Note: host Homo sapiens (man)
C;Date: 17-May-1985 #sequence_revision 17-May-1985 #text_change
C;Accession: A03946
R;Wain-Hobson, S.; Sonigo, P.; Danos, O.; Cole, S.; Alizon, M.
Cell 40, 9-17, 1985
A;Title: Nucleotide sequence of the AIDS virus, LAV.
A;Reference number: A90866; MUID:85099333; PMID:2981635
A;Accession: A03946
                                                                                                                                                                                                                                                                                                                                                 gag polyprotein - human immunodeficiency virus type 1 (strain VU-2)
N;Alternate names: core polyprotein
N;Contains: core protein p15; core protein p17; core protein p24
C;Species: human immunodeficiency virus type 1, HIV-1
A;Note: host Homo sapiens (man)
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 31-Jan-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               F;392-405/Region: zinc finger CCHC motif
F;411-426/Region: zinc finger CCHC motif
F;413-448/Product: core protein p1 #status predicted <CP1>
F;433-448/Product: core protein p6 #status predicted <CP6>
F;449-500/Product: core protein p6 #status predicted <CP6>
F;2/Modified site: myristylated amino end (Gly) (in mature form) #status predicted
F;392,395,400,405/Binding site: zinc (Cys, Cys, His, Cys) #status experimental
F;413,416,421,426/Binding site: zinc (Cys, Cys, His, Cys) #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   F;2-500/Product: gag precursor (assemblin) #status F;2-130/Product: matrix antigen core protein pl7MA F;20-32/Region: nuclear location signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gag polyprotein - human immunodeficiency virus type 1 (isolate LAV-la) N;Alternate names: assemblin; core polyprotein; gag precursor N;Contains: capsid antigen core protein p24CA; core protein p1; core pC;Species: human immunodeficiency virus type 1, HIV-l
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A; Residues: 1-500 <WAI>
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Matches 9; Conserv
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predicted <GAG>
#status predicted <P17>
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KARVLAEAM

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RESULT 11
S33979
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N;Alternate names: core polyprotein
N;Contains: core protein p15; core protein p17; core protein p24
C;Species: human immunodeficiency virus type 1, HIV-1
C;Date: 30-Jun-1988 #sequence_revision 30-Jun-1988 #text_change 16-Jul-1999
C;Accession: A25523
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                                                                                                                          A;Molecule type: mRNĀ
A;Residues: 1-500 <CAR>
A;Cross-references: EMBL:Z11530; NID:g60192; PIDN:CAA77621.1; PID:g60193
C;Superfamily: AIDS-related virus gag polyprotein
                                                                                                                                                                                                                                       R;Carlini, F.
submitted to the EMBL Data
A;Reference number: S33979
A;Accession: S33979
                                                                                                                                                                                                                                                                                                                           gag polyprotein - human immunodeficiency virus type 1
C;Species: human immunodeficiency virus type 1, HIV-1
C;Decies: human immunodeficiency virus type 1, HIV-1
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 26-Aug-1999
C;Accession: S33979
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A; Residues: 1-500 <DES>
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                                                                                                                                                                                                                     A; Status: preliminary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: GB:M13136; NID:g326459; PIDN:AAA44306.1; PID:g326462
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les 9; Conserv
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    2 KARVLAEAM 10
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                                               Similarity
9; Conser
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                                                                 88.9%; Score 40; 100.0%; Pred. No.
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100.0%; Pred. No
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Pred. No.
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predicted <P2
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RESULT 14
T01667
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A; Reference number: S54377
A; Accession: S54377
A; Status: preliminary
A; Molecule type: genomic RNA
A; Residues: 1-501 <THE>
A; Residues: 1-501 <THE>
A; Cross-references: EMBL: M22639; NID:g329377; PIDN:AAA45365.1; PID:g329380
C; Superfamily: AIDS-related virus gag polyprotein
C; Keywords: polyprotein
                                                                                                         R;Alizon, M.; Wain-Hobson, S.; Gluckman, J.C.; Sonigo, P. Cell 46, 63-74, 1986
A;Title: Genetic variability of the AIDS virus: Nucleotide A;Reference number: Z14389; MUID:86245056; PMID:2424612
A;Accession: T01667
                                                                                                                                                                                                                                                                                        gag polyprotein - human immunodeficiency virus type 1
C;Species: human immunodeficiency virus type 1, HIV-1
C;Date: 19-Feb-1999 #sequence_revision 19-Feb-1999 #t
C;Accession: T01667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Gene: gag
C;Superfamily: AIDS-related virus gag polyprotein
C;Keywords: AIDS; core protein; immunodeficiency; po
F;1-134/Product: core protein pl7 *status predicted
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A;Title: Nucleotide sequence and expression of an AIDS-associated retrovirus (ARV-2).
A;Reference number: A04003; MUID:85090453; PMID:2578227
A;Accession: A03947
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N;Contains: core protein p15; core protein p17; core protein p24
C;Species: human immunodeficiency virus type 1, HIV-1
A;Note: host Homo sapiens (man)
C;Date: 17-May-1985 #sequence_revision 17-May-1985 #text_change 16-Jul-1999
C;Accession: A03947
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(;Species: human immunodeficiency virus type 1, HIV-1
C;Date: 15-Jul-1995 #sequence_revision 01-Sep-1995 #t
C;Accession: S54377
R;Theodore, T:; Buckler-White, A.J.
R;Theodore, T:; Buckler-Whit
A;Status: preliminary; translated from GB/EMBL/DDBJA;Molecule type: mRNAA;Residues: 1-505 <ALI>
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A; Residues: 1-502 <SAN>
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Best Local Similarity
Matches 9; Conserv
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Search completed: March Job time: 9.81818 secs

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gag polyprotein - human immunodeficiency virus type 1 (strain MN)
N;Alternate names: core polyprotein
N;Contains: core protein p1; core protein p17; core protein p2; core protein p24; cor
C;Species: human immunodeficiency virus type 1, HIV-1
A;Note: host Homo sapiens (man)
C;Date: 30-Sep-1993 *sequence_revision 30-Sep-1993 *text_change 26-Feb-1999
C;Accession: A38068
R;Henderson, L.E.; Bowers, M.A.; Sowder II, R.C.; Serabyn, S.A.; Johnson, D.G.; Bess
J. Virol. 66, 1856-1865, 1992
A;Title: Gag proteins of the highly replicative MN strain of human immunodeficiency v
A;Accession: A38068
A;Molecule type: protein
A;Residues: 1-506 <HEN>
C;Genetics:
                                                                                                                                                        A;Gene: gag
C;Superfamily: AIDS-related virus gag polyprotein
C;Superfamily: AIDS; core protein; immunodeficiency; polyprotein
C;Keywords: AIDS; core protein p17 #status experimental <P17>
F;1-134/Product: core protein p17 #status experimental <P24>
F;356-379/Product: core protein p2 #status experimental <PP2>
F;380-434/Product: core protein p7 #status experimental <PP2>
F;435-450/Product: core protein p1 #status experimental <PP1>
F;435-450/Product: core protein p6 #status experimental <PP1>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Accession: S72820
R;Smith, D.R.; Robison, K.
submitted to the EMBL Data Library, November 1993
A;Description: Mycobacterium leprae cosmid B1620.
A;Reference number: S72584
A;Accession: S72820
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     hypothetical protein B1620_C3_232 · Mycobacterium leprae
C;Species: Mycobacterium leprae
C;Date: 19-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 23-Mar-2001
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A; Residues: 1-122 <SMI>
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75.0	75.0	75.0	75.0	75.0	75.0	75.0	75.0	75.0	77.3	77.3	77.3	77.3	77.3	77.3	77.3
516	409	397	397	393	386	260	256	126	1527	1513	1361	1224	1163	862	808
N	N	N	N	N	N	N	N	N	_	_	N	N	N	N	N
A31270	E72765	G71031	C75182	S25565	S47163	C69130	н86706	C95270	RN2MB2	RNRZC2	A29959	T07446	S07137	A05028	F70720
radial spoke prote	probable phosphoes	probable DNA-direc	DNA-directed RNA p	DNA-directed RNA p	DNA-directed RNA p	shikimate 5-dehydr	hypothetical prote	hypothetical prote	DNA-directed RNA p	rpoC protein homol	probable transloca				

ALIGNMENTS

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Query Match
Best Local Similarity
Watches 8; Conserve
                                                                                                                                             C;Accession: S72978
R;Smith, D.R.; Robison, K.
submitted to the EMBL Data Library, November 1993
A;Description: Mycobacterium leprae cosmid B229.
A;Reference number: S72588
A;Accession: S72978
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                                                                                A;Cross-references:
C;Genetics:
A;Start codon: GTG
                                                                                                                A; Molecule type: DNA
A; Residues: 1-263 <SMI>
 218
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les 8; Conserv
                   EKARVLAEAA 10
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Pred. No. 2.2;
2; Mismatches
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                                                  Score 38; DB
Pred. No. 4.8;
                                         Mismatches
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                                        Gaps
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A;Title:
                                                                                                                                                                                    50S ribosomal protein L17 nma0102 [imported] - Agrobacterium tumefaciens (strain c):Species: Agrobacterium tumefaciens C:Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 11-Jan-2002 C:Accession: B97591
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    fypothetical protein Rv2585c - Mycobacterium tuberculosis (strain H37RV)
C;Species: Mycobacterium tuberculosis
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 22-Oct-1999
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #seque
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 393, 537-544, 1998
A;Authors: Squares, Taylor, K.; Whitehead, S.; Barrell, B.G. A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete A;Reference number: A70500; MUID:98295987; PMID:9634230
A;Accession: H70725
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A;Authors: Rutter, S.; Seeger, K.; Simon, S.; Simonds, I.A;Authors: Rutter, S.; Seeger, K.; Simon, S.; Simonds, I.A;Authors: Rutter, S.; Seeger, M.; Simon, S.; Simonds, I.A;Artile: Massive ges decay in the leprosy bacillus.
A;Reference number: A86909; MUID:21128732; PMID:11234002
A;Accession: G86956
                                                                                                                                       R;Goodner,
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A; Residues: 1-557 <COL>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Status: preliminary; nucleic acid sequence not shown; translation not
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C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 20-Apr-2001
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A; Residues: 1.281 <STO>
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                                                                                                   A.; Liu,
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218 ERARVVAEAA 227
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nes 8; Conserv
                                                      er, B.; Hinkle, G.; Gattung, S.; u, F.; Wollam, C.; Allinger, M.; 294, 2323-2328, 2001
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les 8; Conserv
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         Plant
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Pred. No. 5
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         Pathogen
                                                                                          Miller, N.; Blanchard, I
Doughty, D.; Scott, C.;
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10;
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Biotechnology
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                                                                                     Scott,
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                                                                                     M.; Qurollo, B.; Gold
; Lappas, C.; Markelz,
    Agent Agrobacterium
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                                                                                     Goldman,
kelz, B.;
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Holroyd,
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                                                                                                                                                                                                                                                                                                                                                                                                                                    probable acetylglutamate kinase (EC 2.7.2.8) NMA1275 [imported] - Neisseria C;Species: Neisseria meningitidis C;Species: Neisseria meningitidis C;Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 02-Feb-2001 C;Accession: G81895 [C;Accession: G81895] [C
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G81895
                                                                                                                                                                                                                                                                                                      A;Title: Complete DNA sequence of a serogroup A strain of A;Reference number: A81775; MUID:20222556; PMID:10761919 A;Accession: G81895
                                                                                                                                                                       A; Molecule type: DNA
A; Residues: 1-298 < PAR>
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                                                                                     A: Experimental source:
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argB; NMA1275

GB:AL157959; NID:g7379742; A, strain Z2491

PIDN:CAB84528.1; PID:g737

Neisseria

menigitidis 22491

Klee, M.A.;

S.R.; Mo Rajandre

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A;Molecule type: DNA
A;Residues: 1-141 <KUR>
A;Cross-references: GB:AE008688; PIDN:AAL42918.1; PID:g17740374; GSPDB:GN00186
A;Experimental source: strain C58 (Dupont)
                                                                                                                                                                                                                                                                                                                                                                                              C;Accession: AH2812
R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, erage, G.; Gillet, W.; Grant, C.; Guenthner, E; Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
                                                                                                                                    A; Map position: circular chromosome C; Superfamily: Escherichia coli ribosomal protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       50S ribosomal protein L17 [imported] - Agrobacterium tumefaciens (strain C5 C;Species: Agrobacterium tumefaciens C;Date: 11-Jan-2002 #sequence_revision il-Jan-2002 #text_change 01-Feb-2002
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AH2812
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                                                                                                                                                                                                                                                                                      A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                 ster, E.W.
                                                                                                                                                                                                                                                                                                                                                                                A; Authors: Yoo, H.;
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A; Residues: 1-141 < KUR>
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A;Accession: B97591
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                                                                    Matches
                                                                                                      Query Match
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                  1 EKARVLAEAA
                                                                                     Local
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                                                                  Similarity
8; Conserv
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8; Conservative
                                                                    Conservative
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                                                                                                                                                                                                                                                                                                                                                                               Y.; Biddle,
                                                                                     81.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            81.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 36;
Pred. No.
                                                                                     Score 36;
Pred. No.
                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           core 36; DB;
red. No. 6.5;
Mismatches
                                                                                                                                                                                                                                                                                                                                                                             P.; Jung, M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Agrobacterium tumefaciens (strain C58,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   protein
                                                                                 DВ
                                                                                                                                                                                                                                                                                                                                                                                                                                  D.; Chen, L.; Wood, G.E.; Chen, D.; Kutyavin, T.; Levy, R.; Li, P
                                                                                                    2
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                                                                                                                                          117
                                                                                                                                                                                                                                                                                                                                                                               Krespan, W.;
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                                                                                                    Length 141;
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                                                                  Gaps
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acetylglutamate kinase NMB1074 [imported] - Neisseria meningitidis (strain MC58 serogrou C;Species: Neisseria meningitidis
C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 19-Jan-2001
C;Accession: E81124
R;Tettelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.P.
Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.;
ri, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Masignani, V.; Pizza, M.
Science 287, 1809-1815, 2000
A;Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; Ve
A;Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58.
A;Reference number: A81000; MUID:20175755; PMID:10710307
A;Accession: E81124
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-298 <TET>
A;Residues: 1-298 <TET>
A;Cross-references: GB:AE002458; GB:AE002098; NID:97226311; PIDN:AAF41469.1; PID:9722631
A;Experimental source: serogroup B, strain MC58
C;Gene: NMB1074
C;Superfamily: acetylglutamate kinase
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Best Local S
                                                                                                                                                                                                                                             gag polyprotein - human immunodeficiency virus type 1 (fragment)
N:Contains: p24 protein; p25 protein; p7 protein
C:Species: human immunodeficiency virus type 1, HIV-1
C:Date: 20-Feb-1995 #sequence_revision 26-Jul-1996 #text_change 26-Aug-1999
C:Accession: S24478; S24484
R:Salminen, M.
submitted to the EMBL Data Library, October 1991
A:Reference number: S24471
A:Reference number: S24471
A:Recession: S24478
A:Molecule type: DNA
A:Residues: 1-75 <SAL>
A:Cross-references: EMBL:Z11148; NID:g60078; PIDN:CAA77499.1; PID:g939876
C:Superfamily: AIDS-related virus gag polyprotein
C:Keywords: polyprotein
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E81124
RESULT 10
S24475
gag polyprotein -
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C; Keywords: phosphotransferase
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11 DKARILAEA 19
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   human
immunodeficiency virus type 1
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77.8%;
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Pred. No. 14;
2; Mismatches
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Pred. No.
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Pred. No.
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14;
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A:Molecule type: DNA
A:Residues: 1-76 <SAL>
A:Residues: 1-76 <SL2:RIP (SAL)
A:Cross-references: EMBL:Z11143; NID:g60103; PIDN:CAA77494.1; PID:g60104
C:Superfamily: AIDS-related virus gag polyprotein
C:Keywords: polyprotein
                                                                                                                                                                                                                                                                                                      RESULT
S24476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gag polyprotein - human immunodeficiency virus type 1
C;Species: human immunodeficiency virus type 1, HIV-1
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 26-Aug-1999
C;Accession: S24474; S24487
R;Salminen, M.
submitted to the EMBL Data Library, October 1991
A;Reference number: S24471
A;Accession: S24474
A;Status: Preliminary
A;Status: Preliminary
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S24474
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C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 26-Aug-1999
C:Accession: S24475; S24488
R:Salminen, M.
submitted to the EMBL Data Library, October 1991
A:Reference number: S24471
                                                                                                                                                 A; Reference number: Si
A; Accession: S24476
A; Status: preliminary
                                                                                                                                                                                                                                                 gag polyprotein - human immunodeficiency virus type 1
C;Species: human immunodeficiency virus type 1, HIV-1
C;Date: 20-Feb-1995 *sequence_revision 20-Feb-1995 *t
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C; Keywords:
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A; Residues: 1-75 <SAL>
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A; Residues: 1-75 <SAL>
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A; Status: preliminary
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8; Conserv
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 Conservative
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2 KARVLAEA 9

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A; Molecule type: DNA
A; Residues: 1-423 <KAW>
A; Cross-references: DDBJ:AP000063; NID:g5105654; PIDN:BAA81210.1; PID:g5105898
A; Experimental source: strain K1
C; Genetics:
A; Gene: APE2199
C; Superfamily: ~--*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Title: Nucleic acid structure and expression of the human AIDS/lymphadenopathy retroview. A;Reference number: A93355; MUID:85111157; PMID:2982104

A;Reference number: A93355; MUID:85111157; PMID:2982104

A;Recession: A03948

A;Molecule type: DNA

A;Residues: 1-478 <MUE>
C;Genetics:
C;Genetics: A;Gene: gag
C;Superfamily: AIDS-related virus gag polyprotein
C;Superfamily: AIDS-related virus gag polyprotein; immunodeficiency; lipoprotein; p;2-478/Product: gag precursor (assemblin) #status predicted <GAG>
F;2-478/Product: matrix antigen core protein p17MA #status predicted <P17>
F:30-23/Enroduct: matrix antigen core protein p17MA #status predicted <P17>
F:30-23/Enroduct: matrix antigen core protein p17MA #status predicted <P17>
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                                                                                                                                                                                                                     F;392-405/Region: zinc finger CCHC motif
F;413-426/Region: zinc finger CCHC motif
F;247Modified site: myristylated amino end (Gly) (in mature form) *status predicted
F;392,395,400,405/Binding site: zinc (Cys, Cys, His, Cys) *status experimental
F;413,416,421,426/Binding site: zinc (Cys, Cys, His, Cys) *status experimental
                                                                                                                                                                                                                                                                                                                                                          F:20-32/Region: nuclear location signal
F:110-114/Region: nuclear location signal
F:133-363-2/Product: capsid antigen core protein p24CA #status predicted <P24>
F:364-377/Product: core protein p2 #status predicted <CP2>
F:378-432/Product: nucleocapsid core protein p7NC #status predicted <CP7>
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N;Alternate names: assemblin; core polyprotein; gag precursor

N;Contains: capsid antigen core protein p24CA; core protein p1; core protein
C;Species: human immunodeficiency virus type 1, HIV-1
C;Date: 17-May-1985 *sequence_revision 17-May-1985 *text_change 05-Dec-1998
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A;Accession: B72528
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  359 KARVLAEA 366
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C;Superfamily: AIDS-related virus gag polyprotein C;Keywords: AIDS; core protein; immunodeficiency; polyprotein F;1-129/Product: core protein p17 *status predicted <C17> F;130-389/Product: core protein p24 *status predicted <C24> F;390-497/Product: core protein p15 *status predicted <C15>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gag polyprotein - human immunodeficiency virus type 1 (isolate NDK)

R/Alternate names: core polyprotein

N/Contains: core protein pl5; core protein pl7; core protein p24

C/Species: human immunodeficiency virus type 1, HTV-1

A/Note: host Homo sapiens (man)

C/Date: 30-Sep-1991 *sequence_revision 30-Sep-1991 *text_change 16-Jul-1999

C/Accession: J00065

R/Spire, B.; Sire, J.; Zachar, V.; Rey, F.; Barre-Sinoussi, F.; Galibert, F.;

Gene 81, 275-284, 1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Title: Nucleotide sequence of HIV1-NDK: a highly cytopathic strain of the human imm A;Reference number: JQ0065; MUID:90034200; PMID:2806917 A;Accession: JQ0065 A;Bolecule type: DNA A;Residues: 1-497 <SPI> A;Cross-references: GB:M27323; NID:g328154; PIDN:AAA44868.1; PID:g328157
Search completed: March Job time: 11.8182 secs
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 GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
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7 Q9HGZ8
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Q921e1 rhizobium m
Q49726 mycobacteri
Q49858 mycobacteri
Q9ccv3 mycobacteri
Q9ck21 homo sapien
Q9hyz8 pyrococcus
Q8ue41 agrobacteri
O92na6 rhizobium m
Q9j122 human immun
Q9j1181 human immun
Q9j140 human immun
Q9j140 human immun
Q9j144 human immun
Q9j144 human immun
Q9j144 human immun
Q9j138 human immun
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Q92L
ID Q92L
AC Q92L
DT 01-D
DT 01-M
DT 01-M
DT Puta
GN TRM2
OC Bact
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Q9j125 hur Q97597 hur	127	173	175	186	115	120	136 1	137	139	147	158	160	171	174	195	155	159	167	182	184	189	123	126	j177	-1	Q9j132 human	j 168
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•		90.9%; Score 40; DB 16; Length 152; 80.0%; Pred. No. 3.4; vative 2; Mismatches 0; Indels 0; Gaps	152 AA; 16544 MW;	Pfam; PF01527; Transposase_8; 1.	InterPro: IDR002514: Transposase 8	Proc. Natl. Acad. Sci. U.S.A. 98:9877-9882(2001).	Sinorhizobium meliloti strain 1021.";	*Analysis of the chromosome sequence of the legume symbiont	Renard C., Thebault P., Vandenbol M., Weidner S., Galibert F.;	Pohl T. Portetelle D. Puehler A. Purnelle B. Ramsperger U.	Godrie T., Goffeau A., Kahn D., Kiss E., Lelaure V., Masuv D.,	Capela D., Barloy-Hubler F., Gouzy J., Bothe G., Ampe F., Batut J.,	MEDLINE=21396507; PubMed=11481430;	STRAIN-1021;	SEQUENCE FROM N.A.	[1]	NCBI_TaxID=382;	Rhizobiaceae; Sinorhizobium.	Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;	Rhizobium meliloti (Sinorhizobium meliloti).	TRM28.1 OR R03124 OR SMC03278.	ansposase number 1 for insertion sequence	(TrEMBLrel. 20,	(TrEMBLrel. 19,	2001	TREFFEMINARY; TRIT	

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Q49838;
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O1-NOV-1996 (TrEMBLrel. 01, Created)
O1-NOV-1996 (TrEMBLrel. 01, Last sequence update)
O1-FEB-1997 (TrEMBLrel. 02, Last annotation update)
O1-FEB-1997 (TrEMBLrel. 02, Last annotation update)
Hypothetical 27.4 kDa protein B229_C1_175 precursor
B229_C1_175.
Q9CCV3;
Q9CCV3;
01-JUN-2001
01-JUN-2001
                                                                                                                                                                                                      smith D.R., Robison K.; Submitted (MAR-1994) to the EMBL/GenBank/DDBJ databases.-I-SIMILARITY: STRONG, TO M.TUBERCULOSIS MTCY78.14.
EMBL, U00020; AAA17292.1; -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mycobacterium leprae.
Mycobacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Bacteria; Firmicutes; Actinobacteria; Mycobacteriaceae; Mycobacterium.
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Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Corynebacterineae; Mycobacteriaceae; MCBI_TaxID=1769;
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Submitted (MAR-1994) to the
-!- SIMILARITY: STRONG, TO N
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01-FEB-1997 (TrEMBLrel.
Hypothetical 12.9 kDa pr
B1620_C3_232.
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01-NOV-1996
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264 AA;
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ilarity 80.0%;
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Created)
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Pred. No. 6.8;
2; Mismatches
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Pred. No.
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HYPOTHETICAL PROTEIN B229_C1_175;
7BBA3900F8911DF4 CRC64;
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Strausberg R.;
Submitted (OCT-2001) to the EMBL/Genounce,
REMBL; AK027746; BAB55338.1; -.
REMBL; BC015738; AAH15738.1; -.
RINterpro; IPR000564; 2Fe2Ferredoxin.
DR Interpro; IPR000345; CytC_heme_bind.
DR Interpro; IPR000306; Znf_FYVE.
DR Interpro; IPR000306; Znf_FYVE.
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Isogai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y., Nishikawa T., Nagai K., Sugano S., Shiratori A., Sudo H., Nishikawa T., Nagai K., Sugano S., Shiratori A., Sudo H., Sugawara M., Wagatsuma M., Hosoiri T., Kaku Y., Kodaira H., Kondo H., Sugawara M., Wagatsuma M., Chiba Y., Ishida S., Murakawa K., Ono Y., Takiguchi S., Watanabe S., Kimura K., Murakami K., Ishii S., Kawai Y., Saito K., Yamamoto J., Wakamatsu A., Nakamura Y., Nagahari K., Masuho Y., Ninomiya K., Iwayanagi T.;

"NEDO human cDNA sequencing project.";
Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q96K21 PRELIMINARY; PRT; 396 AA. Q96K21; Q1-DEC-2001 (TrEMBLrel. 19, Created) 01-DEC-2001 (TrEMBLrel. 19, Last sequence update) 01-MAR-2002 (TrEMBLrel. 20, Last annotation update) CDNA FLJ14840 fis, clone OVARC1001916 (Hypothetical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-1128732; PubMed-11234002;
MEDLINE-1128732; PubMed-11234002;
Cole S.T., Eiglmeier K., Parkhill J., James K.D., Thomson N.R.,
Wheeler P.R., Honore N., Garnier T., Churcher C., Harris D.,
Wingall K., Basham D., Brown D., Chillingworth T., Connor R.,
Mungall K., Basham D., Brown D., Chillingworth T., Fraser A., Hemlin N.
Holroyd S., Hornsby T., Jagels K., Lacrolx C., Maclean J., Moule S.,
Holroyd S., Hornsby T., Jagels K., Lacrolx C., Maclean J., Moule S.,
Murphy L., Oliver K., Ouail M.A., Rajandream M.A., Rutherford K.M.,
Rutter S., Seeger K., Simon S., Simmonds M., Skelton J., Squares R.,
Squares S., Stevens K., Taylor K., Whitehead S., Woodward J.R.,
                                                                                                                                                                                                                                                                                                                                                                                                          protein).

Homo sapiens (Human).

Homo sapiens (Human).

Theria; Primates;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-OCT-2001 (TrEMBLrel 18, Hypothetical protein ML0383.ML0383.
                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
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Bacteria; Firmicutes; Actinobacteria;
                                                                                                                                                         TISSUE-RETINA;
                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=9606;
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8; Conserv
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           2FE2S_FERREDOXIN; UNKNOWN_1.
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Pred. No.
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Catarrhini; Hominidae;
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FE0AlBDCFD69803F CRC64;
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Q9HGZ8;
                                                                                                                                                        Q8UE41;
01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation updat
50s ribosomal protein L17.
RPLQ OR ATU1922 OR AGR_C_3516.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SPECIES-P.furiosus; STRAIN-VC1 / DSM 3638 / ATCC 43587 / JCM Weiss R.B., Dunn D.M., Robb F.T., Brown J.R.; "The complete sequence of the Pyrococcus furiosus genome.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-MAR-2001 (TrEMBLrel. 16, 01-MAR-2001 (TrEMBLrel. 16, 01-JUN-2002 (TrEMBLrel. 21, Hypothetical protein PF1746
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hypothetical SEQUENCE 3
                                                                                                             Agrobacterium tumefaciens (strain C58 / ATCC Bacteria; Proteobacteria; alpha subdivision;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mol. Microbiol. 38:684-693(2000).
EMBL; AE010273; AAL81870.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Diruggiero J., Dunn D., Maeder D.L., Hol
Horlacher R., Robb F.T., Boos W., Weiss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SPECIES-P.furiosus, and T.litoralis; MEDLINE-20566786; PubMed-11115105;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE; PS00190; CYTOCHROME_C; UNKNOWN_1.
SEQUENCE FROM N.A. MEDLINE-21608550;
                                                                                          Rhizobiaceae;
                                                                                                                                                                                                                                                                                                  Q8UE41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Horlacher R., Robb F.T., Boos W., Weiss R.B., 
"Evidence of recent lateral gene transfer among
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (FEB-2002)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Archaea; Euryarchaeota; Thermococci;
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                                                                                                                                                                                                                                                                                                                                                                                                                    531
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AF307052; AAG45379.1;
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B; Conserv
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396 AA; 4
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637 AA; 72701 MW; EBFA42F42FB5A428 CRC64;
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                                                                                          Rhizobium
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  PubMed-11743193;
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Last sequence update)
Last annotation update)
(Hypothetical 72.7 kDa |
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                                                                                                                                                                                                                                                                                               PRT;
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                                                                                                                                                                                                                                                                                               141
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                                                                                                               ATCC 33970).
sion; Rhizobiaceae
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 637;
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Q1-DEC-2001 (TrEMBLrel. 19, Created)
O1-DEC-2001 (TrEMBLrel. 19, Last sequence update)
O1-DEC-2001 (TrEMBLrel. 20, Last annotation update)
O1-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Hypothetical protein R02307.
R02307 OR SMC01556.
Rhizobium meliloti (Sinorhizobium meliloti).
Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Goodner B., Hinkie G., Gattung S., Miller N., Blanchard M., Qurollo B., Goldman B.S., Cao Y., Askenazi M., Halling C., Mullin Houmiel K., Gordon J., Yaudin M., Iartchouk O., Epp A., Liu F., Wollam C., Allinger M., Doughty D., Scott C., Lappas C., Markelz Flanagan C., Crowell C., Gurson J., Lomo C., Sear C., Strub G., Cielo C., Slater S.;
"Genome sequence of the plant pathogen and biotechnology agent Agrobacterium tumefaciens C58.";
Science 294:2323-2328(2001).
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                                                                                                                                                                 Capela D., Barloy-Hubler F., Gouzy J., Bothe G., Ampe F., Batut Boistard P., Becker A., Boutry M., Cadleu E., Dreano S., Gloux Godrie T., Goffeau A., Kahn D., Kiss E., Lelaure V., Masuy D., Pohl T., Portetelle D., Puehler A., Purnelle B., Ramsperger U., Renard C., Thebault P., Vandenbol M., Weidner S., Galibert F.; "Analysis of the chromosome sequence of the legume symbiont Sinorhizoblum meliloti strain 1021.", Proc. Natl. Acad. Sci. U.S.A. 98:9877-9882(2001).
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                                                                                                                 Hypothetical protein; Complete SEQUENCE 262 AA; 27103 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-21396507; PubMed-11481430;
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986D78DE6DDE79F2 CRC64;
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EMBL; AF219292; AAF30198.1; -.
HSSP; P05888; IAAF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Liltsola K., Holmstrom P., Laukkanen T., Brummer-Korvenkont:
Leinikki P., Salminen M.O.;
"Analysis of HIV-1 genetic subtypes in Finland reveals good
correlation between molecular and epidemiological data.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR001878; znf_CCHC.
Pfam; PF00098; zf-CCHC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Viruses; Retroid viruses; Retroviridae; NCBI_TaxID=11676;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gag protein GAG.
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                                                                                                                                                          Score 35; DB;
; Pred. No. 12;
0; Mismatches
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Q9J140;
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EMBL; AF219356; AAF30262.1;
HSSP; P05888; 1AAF.
                                                                                                                                                                                                                                                               Liitsola K., Holmstrom P., Laukkanen T., Brummer-K
Leinikki P., Salminen M.O.;
"Analysis of HIV-1 genetic subtypes in Finland rev
correlation between molecular and epidemiological
Scand. J. Infect. Dis. 0:0-0(2000).
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pfam; pf00098; zf-CCHC; 1.
SMART; SM00343; znf_C2HC; 1.
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Leinikki P., Salminen M.O.;
"Analysis of HIV-1 genetic subtypes in Finland reveals good
correlation between molecular and epidemiological data.";
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Pfam; PF00098; zf-CCHC; 1.
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                                                                                                                                                         SMART; SM00343; ZnF_C2HC; 1.
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8; Conserv
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8; Conserv
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AA;
  Conservative
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6191 MW;
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79.5%; Score 35;
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Pred. No.
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Q9J144;
Q1-OCT-2000
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01-OCT-2000
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Q9J138;
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SEQUENCE
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"Analysis of HIV-1 genetic subtypes in correlation between molecular and epide Scand. J. Infect. Dis. 0:0-0(2000).
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Leinikki P., Salminen M.O.;
"Analysis of HIV-1 genetic subtypes in Finland reveals good
correlation between molecular and epidemiological data.";
Scand. J. Infect. Dis. 0.0-0(2000).
EMBL; AF219329; AAF30235.1;
HSSP; P05886; IAAF.
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Pfam; PF00098; zf-CCHC; 1.
SMART; SM00343; Znf_C2HC; 1.
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Viruses; Retroid viruses; Retroviridae;
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HSSP; P05888; 1AAF.
InterPro; ITR001878; Znf_CCHC.
Pfam; PF00098; Zf-CCHC; 1.
SMART; SM00343; ZnF_C2HC; 1.
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Local Similarity 100.0%;
hes 8; Conservative (
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Retroviridae; Lentivirus
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DB 15; Length 58;
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"Analysis of HIV-1 genetic subtypes i correlation between molecular and epi Scand. J. Infect. Dis. 0:0-0(2000). EMBL; AF219275; AAF30181.1; -. HSSP; P0588; IAAF.
InterPro; IPR001878; Znf_CCHC.
Pfam; PP00098; Zf-CCHC; 1.
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Viruses; Retroid viruses; Retroviridae;
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    DB
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	or send an email to license@isb-sib.ch).	entities requires a license agreement (See http://www.isb-sib.ch/announce/	9	European Bioinformatics Institute. There are no restrictions on	between the Swiss Institute of Bioinformatics and the EMBL outstation -	This SWISS-PROT entry is copyright. It is produced through a collaboration		-!- SUBCELLULAR LOCATION: Attached to the membrane by a lipid anchor	mitted (APR-2001) to the EMBL/GenBank/DDBJ database	laboratory strains.";	"Whole genome comparison of Mycobacterium tuberculosis clinical and		J., Mikula	Kolonav J. F. Nelson W.C. Umavam L.A. Ermolaeva M.D. Salzberg S.L.	presson T. DeBoy R. Dodson R. Gwinn M. Haft D. Hickey F.	Cassostos I white	SECULENCE FROM N.A.	Nature 393:537-544(1998).		"Deciphering the biology of Mycobacterium tuberculosis from the	uttet o., seeget o., skettom s., squares s., squares k.,	CHIVEL 3. CAROLIE d., Qualt m.A., Rejandream m.A., Royers d.,	Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,	avies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S.,	Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,	meier K., Gas S., Barry C.E. III, Tekaia F.,	Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,	MEDLINE-98295987; PubMed-9634230;	SEQUENCE FROM N.A.	[1]	NCBI_TaxID=1773;	Actinomycetales; Corvnebacterineae; Mycobacteriaceae; Mycobacterium.		7.16.	prote	ati	01-NOV-1997 (Rel. 35, Creaced)	y n	YP85_MYCTU STANDARD; PRT; 557 AA.	ת 1	

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                                                                                                                                                                                                                                                                    the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Nature 404.502-506(2000).
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InterPro; IPR004662; AcgluKinase.
InterPro; IPR001057; Glu_5kinase.
Pfam; PF00696; Bakknase; 1.
PRINTS; PR00474; GLU5KINASE.
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Bacteria; Proteobacteria; beta suk
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15-JUN-2002 (Rel. 41, Last sequence up
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Acetylglutamate kinase (EC 2.7.2.8) (N
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glutamate 5-phosphate.
PATHWAY: Arginine blosynthesis; second step.
SUBCELLULAR LOCATION: Cytoplasmic (Potential).
SIMILARITY: BELONGS TO THE ACETYLGLUTAMATE KINASE FAMILY.
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01-FEB-1994
16-OCT-2001
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SEQUENCE FROM N.A.

STRAIN-MC58 / Serogroup B;

MEDLINE-20175755: PubMed-10710307;

Tettelin H., Saunders N.J., Heidelberg J., Jeffries A.C., Nelson K.E.,

Tettelin H., Saunders N.J., Heidelberg J., Jeffries A.C., Nelson R.J.,

Reisen J.A., Ketchum K.A., Hood D.W., Peden J.F., Dodson R.J.,

Nelson W.C., Gwinn M.L., DeBoy R., Peterson J.D., Hickey E.K.,

Haft D.H., Salzberg S.L., White O., Fleischmann R.D., Dougherty B.A.,

Mason T., Clecko A., Parksey D.S., Blair E., Cittone H., Clark E.B.,

Cotton M.D., Utterback T.R., Khourl H., Qin H., Vamathavan J.,

Smith H.O., Fraser C.M., Moxon E.R., Rappuoli R., Venter J.C.;

"Complete genome sequence of Neisseria meningitidis serogroup B strain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a between the Swiss Institute of Bioinformatics and the EMBI the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and modified and this statement is not removed.
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-I- PATHWAY: Arginine blosynthesis; second step.
-I- SUBCELLULAR LOCATION: Cytoplasmic (Potential).
-I- SIMILARITY: BELONGS TO THE ACETYLGLUTAMATE KINASE FAMILY.
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PRINTS; PR00474; GLUSKINAS;
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ArgInine biosynthesis; Transferase; Kinase; Complete proteome SEQUENCE 298 AA; 31283 MW; 7A19DFE8D5BA1A74 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Acetylglutamate kinase (EC 2.7.2.8) (NAG kina
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AE002458; AAF41469.1; -. TIGR; NMB1074; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Science 287:1809-1815(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Neisseria meningitidis (serogroup
Bacteria; Proteobacteria; beta sul
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID-491;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ARGB OR NMB1074.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pro; IPR001048; Aa_kinase.
Pro; IPR004662; AcgluKinase.
Pro; IPR001057; Glu_5kinase.
Pr00696; aakinase; 1.
                                                                                                                                                                                                                                                                                                                           Similarity 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5-phosphotransferase).
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                                                                                                    STANDARD;
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28,
40,
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77.8%;
Created)
Last sequence
Last anno
sequence up
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Pred.
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                                                                                                                                                                                                                                                                                                                                Mismatches
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                         update)
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6.3;
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                                                                                                                                                                                                                                                                                                                                                                         Length 298;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               restrictions
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update)

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GAG_HYUM
ID GAG_H
ID GAG_H
AC P2473
DT 01-FA
DT 15-JU
DE GAG_E
GN GAG_E
OS HUMAN
OC Virus
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                                                                                                                                                                        Query Match
Best Local S
Matches
                                               01-MAR-1992
01-FEB-1994
15-JUN-2002
                                                                           GAG_HV1U4
P24736;
                                                                                                                                                                                                                                           CHAIN
CHAIN
                                                                                                                                                                                                                                                                                                                                                                                    the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                        LIPID
NON_TER
                                                                                                                                                                                                                                                              CHAIN
                                                                                                                                                                                                                                                                                                                               HSSp, P03351; BEIA.
HIV: K03457; GAG$WMJ2.
InterPro; IPR000721; Gag_p24.
InterPro; IPR000071; Retrovir_p17.
                                                                                                                                                                                                                                                                                                                                                            EMBL; K03457; AAB12988.1; -. HSSP; P03351; 1EIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human immunodeficiency virus type 1 (WMJ2 isolate) Viruses; Retroid viruses; Retroviridae; Lentivirus
                  Human immunodeficiency virus type 1 (strain Ugandan
                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                          CHAIN
                                                                                                                                                                                                                                                                                          Zinc-finger.
                                                                                                                                                                                                                                                                                                     AIDS;
                                                                                                                                                                                                                                                                                                                        Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                          between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GRG polyprotein [Contains: Core proteins P17, P24,
          (HIV-1).
                                                                                                                                    358
                                                                                                                                                                                                                                                                                    CNIT MET
                                                                                                                                                      N
                                     polyprotein
                                                                                                                                    KARVLAEA 365
                                                                                                                                                      KARVLAEA 9
                                                                                                                                                                                                                                                                                                                                                                                                                                       SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                             PF00540; Gag_p17; 1.
PF00607; Gag_p24; 1.
                                                                                                                                                                                                                                                                                                     Core protein;
                                                                                                                                                                         Similarity
8; Conser
Retroid viruses; Retroviridae; Lentivirus
                                                                                                                                                                                                             388
388
                                    (Rel. 21 Created)
(Rel. 28, Last sequence update)
(Rel. 41, Last annotation update)
tein [Contains: Core proteins P17,
                                                                                                                                                                                                                                          0
1
132
363
377
                                                                                                                                                                         Conservative
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                                                                                    STANDARD;
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131
362
376
>388
                                                                                                                                                                                                               43314
                                                                                                                                                                                                                                                                                                    Polyprotein; Myristate; Phosphorylation;
                                                                                                                                                                                  79.5%; Score 35; 100.0%; Pred. No.
                                                                                                                                                                                                              WW;
                                                                                                                                                                         0;
                                                                                                                                                                                                                                         BY SIMILARITY.

CORE PROTEIN P17 (MATRIX PROTEIN).

CORE PROTEIN P24 (CORE ANTIGEN).

CORE PROTEIN P2.

CORE PROTEIN P7 (NUCLEOCAPSID PROTEIN).
                                                                                                                                                                                                                                  MYRISTATE
                                                                                                                                                                                                               EF885BE10ECF7804 CRC64;
                                                                                                                                                                         Mismatches
                                                                                    492
                                                                                                                                                                                  DB 1;
. 13;
                                                                                                                                                                                                                                 (BY SIMILARITY).
                                                                                    A
                                     P24,
                                                                                                                                                                        0
                                                                                                                                                                                            Length 388;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          P2,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (HIV-1).
                                     P2,
                   / isolate U455)
                                     ₽7,
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                                      Ρ1,
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Best Local S
Matches 8
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pfam; PF00540; Gag_p217; 1.

Pfam; PF00607; Gag_p24; 1.

Pfam; PR00607; Gag_p24; 1.

PRINTS; PR00939; CZHCZNFINGER.

PRINTS; PR00234; HYVIMATRIX.

SMART; SM00343; ZNF_CZHC; 2.

PROSTTE; PS50158; ZF_CCHC; 2.

AIDS; Core protein; Polyprotein; M.
                                 GAG_HYIND STANDARD,
GAG_HYIND STANDARD,
p18800;
p18800;
p1. Apple (Rel. 16, Created)
01-ROY-1990 (Rel. 28, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
15-JUN-2002 (Rel. 41, Contains: Core proteins P17, P24, P2, P7,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CHAIN
CHAIN
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ZN_FING
ZN_FING
LIPID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
MEDLINE-91090981; PubMed-2265025;
Oram J.D., Downing R.G., Roff M., Clegg J.C.S.,
Human immunodeficiency virus type 1 (NDK isolate) (HIV-1). Viruses; Retroid viruses; Retroviridae; Lentivirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AIDS; Core protein;
Zinc-finger; Repeat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR000721; Gag_p24.
InterPro; IPR000071; Retrovir_p17.
InterPro; IPR001878; Inf_CCHC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; M62320; AAA75018.1; -. HSSP; P05888; 1AAF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Carswell J.W.;
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                                                                                                                                                                                                                                                                                 354 KARVLAEA
                                                                                                                                                                                                                                                                                                                          2 KARVLAEA 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PTM: THE P24 PROTEIN IS PHOSPHORYLATED. SIMILARITY: CONTAINS 2 CCHC-TYPE ZINC FINGERS.
                                                                                                                                                                                                                                                                                                                                                                     Similarity
8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                           492
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359
372
426
442
383
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358
371
425
441
492
400
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                                                                                                                                                                                                                                                                                                                                                                       0;
                                                                                                                                                                                                                                                                                                                                                                   Score 35; DB Pred. No. 16; 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                         CCHC-TYPE 1.
CCHC-TYPE 2.
CCHC-TYPE 2.
MYRISTATE (BY SIMILARITY).
E4A3B4D633BB6972 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORE
CORE
CORE
CORE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Myristate;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROTEIN P7.
PROTEIN P1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROTEIN
PROTEIN
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                                                                                                                                                                                                                                                                                                                                                                                       DB
16;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (NUCLEOCAPSID PROTEIN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (MATRIX PROTEIN) (CORE ANTIGEN).
                                                                                                                                                                                                                                                                                                                                                                       0;
                                                                                                                                                                                                                                                                                                                                                                                                                Length 492;
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RESULT 7
GAG_HV10Y
ID GAG_H
AC P2088
DT 01-FE
DT 01-FE
DT 115-JU
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Best Local S
Matches 8
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InterPro; IPRO0071; Retrovir_p17.
InterPro; IPRO01878; Znf_CCHC.
Pfam; PF00098; zf-CCHC; 2.
Pfam; PF00540; Gag_p17; 1.
Pfam; PF00607; Gag_p24; 1.
Pfam; PF00607; Gag_p24; 1.
PFNNTS; PR00939; CZHCZNFINGER.
PRINTS; PR00934; INTUMATRIX.
SMART; SM00343; ZnF_CCHC; 2.
PROSITE; PS50158; ZF_CCHC; 2.
GAG_HY1OY STANDARD: PRT; 498 AA. P20889; O1-FEB-1991 (Rel. 17, Created) O1-FEB-1994 (Rel. 28, Last sequence update) 15-JUN-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                         ZN_FING
LIPID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                    CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; M27323; AAA44868.1; -. PIR; J00065; FOLUND. HSSP; P05888; IAAF. HIV; M27323; GAG$NDK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gene 81:275-284(1989)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Nucleotide sequence of HIV1-NDK: a highly cytopathic strain of the human immunodeficiency virus.";
Gene 81:275-284/1000\
                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                    CHAIN
                                                                                                                                                                                                                                                                                                                               CHAIN
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                                                                                                                                                                                                                                                                                                                                                                                                 AIDS; Core pr
Zinc-finger;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=90034200; PubMed=2806917;
Spire B., Sire J., Zachar V., Rey
Hampe A., Chermann J.C.;
                                                                                                                                                                                                                                                                                                                                              CHAIN
                                                                                                                                                                                                                                                                                                                                                           CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=11695;
[1]
                                                                                                                                 355
                                                                                                                                                            N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FUNCTION: PERFORMS HIGHLY COMPLEX ORCHESTRATED TASKS DURING THE ASSEMBLY, BUDDING, MATURATION, AND INFECTION STAGES OF THE VIRAL REPLICATION CYCLE. DURING VIRAL ASSEMBLY, THE PROTEINS FORM MEMBRANE ASSOCIATIONS AND SELF-ASSOCIATIONS THAT ULTIMATELY RESULT IN BUDDING OF AN IMMATURE VIRION FROM THE INFECTED CELL. GAG PRECURSORS ALSO FUNCTION DURING VIRAL ASSEMBLY TO SELECTIVELY BIND AND PACKAGE TWO PLUS STRANDS OF GENOMIC RNA.

MISCELLANEOUS: NDK, ISOLATED FROM A ZAIRIAN PATIENT AFFECTED WITH AIDS, AND IS A HIGHLY CYTOPATHOGENIC STRAIN.

SIMILARITY: CONTAINS 2 CCHC-TYPE ZINC FINGERS.
                                                                                                                                KARVLAEA 362
                                                                                                                                                            KARVLAEA 9
                                                                                                                                                                                     l Similarity
8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                              protein;
                                                                                                                                                                                                                                             496
                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                 Repeat.
                                                                                                                                                                                                                                            ξ,
                                                                                                                                                                                                                                                                      128
359
374
429
445
496
404
                                                                                                                                                                                                                                                                                                                                                                                                              Polyprotein; Myristate; Phosphorylation;
                                                                                                                                                                                                                                            55152
                                                                                                                                                                                                  79.5%;
                                                                                                                                                                                                                                            3
                                                                                                                                                                                     0;
                                                                                                                                                                                                                                                                     CORE PROTE
CORE PROTE
CCHC-TYPE
CCHC-TYPE
                                                                                                                                                                                                  Score 35;
Pred. No.
                                                                                                                                                                                                                                           MYRISTATE (BY SIMILARITY).
F50A42E42CCF20AA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rey F., Barre-Sinoussi F., Galibert F.,
                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                     SIMILARITY.
                                                                                                                                                                                                                                                                                                 E PROTEIN P17
E PROTEIN P24
E PROTEIN P2.
E PROTEIN P7 ()
E PROTEIN P1.
E PROTEIN P6.
                                                                                                                                                                                                   DB 1;
16;
                                                                                                                                                                                                                                                                                                                            (NUCLEOCAPSID PROTEIN).
                                                                                                                                                                                     0
                                                                                                                                                                                                                                                                                                                                                        (MATRIX PROTEIN) (CORE ANTIGEN).
                                                                                                                                                                                                             Length 496;
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RESULT 8
GAG_HV1C4
ID GAG_H
AC P0588
DT 01-NO
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Best Local
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InterPro; IPR00071; Retrovir_p17.
InterPro; IPR00078; Znf_CCHC.
InterPro; IPR00078; Znf_CCHC; 2.
Pfam; PF00098; Zf-CCHC; 2.
Pfam; PF00540; Gag_p17; 1.
Pfam; PF00540; Gag_p24; 1.
Pfam; PF00607; Gag_p24; 1.
Pfam; PF00607; Gag_p24; 1.
PRINTS; PR00939; CZHC:NFINGER.
PRINTS; PR00934; HIVIMATRIX.
SMART; SM00343; ZnF_CCHC; 2.
AIDS; Core Protein; Polyprotein; Myr
AIDS; Core Protein; Polyprotein; Myr
GAG_HV1C4 STANDARD;
P05887;
01-NOV-1988 (Rel. 09, Created)
                                                                                                                                                                                                                                    ZN_FING
ZN_FING
LIPID
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                                                                                                                                                                                                                                                                                                                         CHAIN
                                                                                                                                                                                                                                                                                                                                                                             AIDS; Core protein;
Zinc-finger; Repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; M26727; AAA83391.1; -. HSSP; P05888; 1AAF. HIV; M26727; GAGSOYI.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Huet T., Dazza M.C., Brun-Vezinet F., Roelants A highly defective HIV-1 strain isolated from individual presenting an atypical western blot. AIDS 3:707-715(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GAG
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                                                                                                                                                                                                                                                                               CHAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human immunodeficiency virus type 1 (OYI isolate) (HIV-1). Viruses; Retroid viruses; Retroviridae; Lentivirus.
                                                                                                       358
                                                                                                                        2 KARVLAEA 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FUNCTION: PERFORMS HIGHLY COMPLEX ORCHESTRATED TASKS DURING THE ASSEMBLY, BUDDING, MATURATION, AND INFECTION STAGES OF THE VIRAL REPLICATION CYCLE. DURING VIRAL ASSEMBLY, THE PROTEINS FORM MEMBRANE ASSCCIATIONS AND SELF-ASSCCIATIONS THAT ULTIMATELY MEMBRANE ASSCCIATIONS AND SELF-ASSCCIATIONS THAT ULTIMATELY RESULT IN BUDDING OF AN IMMATURE VIRION FROM THE INFECTED CELL. GAG PRECURSORS ALSO FUNCTION DURING VIRAL ASSEMBLY TO SELECTIVELY BIND AND PACKAGE TWO PLUS STRANDS OF GENOMIC RNA.

PTM: THE P24 PROTEIN IS PHOSPHORYLATED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HEALTHY GABONESE INDIVIDUAL.
SIMILARITY: CONTAINS 2 CCHC-TYPE ZINC FINGERS.
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8; Conser
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CCHC-TYPE 1.
CCHC-TYPE 2.
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                                                                                                                                                                                                                      BDFF20658DEB20B1 CRC64;
                                                                                                                                                               Mismatches
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E PROTEIN P24
E PROTEIN P2.
                                                                                                                                                                                                                                                                                                                                                                                               Myristate;
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No.
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(See http://www.isb-sib.ch/announce/
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P6.
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a healthy Gabonese
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Best Local
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InterPro; IPR000721; Gag_p24.
InterPro; IPR000721; Retrovir_p17.
InterPro; IPR001878; Znf_CCHC.
Pfam; PF00098; Zrf-CCHC; 2.
Pfam; PF00540; Gag_p17; 1.
Pfam; PF00540; Gag_p24; 1.
Pfam; PF00540; Gag_p24; 1.
Pfam; PF00540; Gag_p26; 2.
PRINTS; PR00939; C2HCZNFINGER.
PRINTS; PR00934; HIVIMATRIX.
SMART; SM00343; ZnF_C2HC; 2.
PROSITE; PS50158; ZF_CCHC; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Molecular cloning and primary nucleotide sequence analysis of a distinct human immunodeficiency virus isolate reveal significant divergence in its genomic sequences."; proc. Natl. Acad. Sci. U.S.A. 83:8380-8884(1986).

-1- FUNCTION: PERFORMS HIGHLY COMPLEX ORCHESTRATED TASKS DURING THE ASSEMBLY, BUDDING, MATURATION, AND INFECTION STAGES OF THE VIRAL REPLICATION CYCLE. DURING VIRAL ASSEMBLY, THE PROTEINS FORM MEMBRANE ASSOCIATIONS AND SELF-ASSOCIATIONS THAT ULTIMATELY RESULT IN BUDDING OF AN IMMATURE VIRION FROM THE INFECTED CELL. GAG PRECURSORS ALSO FUNCTION DURING VIRAL ASSEMBLY TO SELECTIVELY BIND AND PACKAGE TWO PLUS STRANDS OF GENOMIC RNA.

-1- PTM: THE P24 PROTEIN IS PHOSPHORYLATED.

-1- SIMILARITY: CONTAINS 2 CCHC-TYPE ZINC FINGERS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and: for contities requires a license agreement (See http://www.isb-sib.ch/ar
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MEDLINE-87041461; PubMed-3490666;
Desai S.M., Kalyanaraman V.S., Casey J.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-FEB-1994 (Rel.
15-JUN-2002 (Rel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   entities requires a license agreement (See http://www.isb-sib.ch/announce, or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human immunodeficiency virus type 1 (CDC-451 isolate) (HIV-1).
Viruses; Retroid viruses; Retroviridae; Lentivirus.
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                                                                                                                      SEQUENCE
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                              2 KARVLAEA 9
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KARVLAEA 365
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8; Conserv
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    28, Last sequence update)
    41, Last annotation update)
    (Contains: Core proteins P17,

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362
376
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                                                                                                                      55796
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CORE PROTEIN P24 (CORE ANTIGEM).

CORE PROTEIN P2.

CORE PROTEIN P2.

CORE PROTEIN P1 (NUCLEOCAPSID PROTEI

CORE PROTEIN P1.
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                                                                                                                  CCHC-TYPE 1.
CCHC-TYPE 2.
CCHC-TYPE 2.
MYRISTATE (BY SIMILA
WYRISTATE (BY SIMILA
                                                                         Score 35; Pred. No.
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16;
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19C6F22AD CRC64;
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                                                                                      Length 499;
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Pfam; PF00540; Gag_p17; 1.
Pfam; PF00607; Gag_p24; 1.
PRINTS; PR00939; C2HCZNFINGER.
PRINTS; PR00939; C2HCZNFINGER.
PRINTS; PR00234; HYVLMATRIX.
SMART; SM00343; ZnF_C2HC; 2.
PROSITE; PS50158; ZF_CCHC; 2.
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13-AUG-1987
01-FEB-1994
15-JUN-2002
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ZN_FING
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-86245056; PubMed-2424612;
MEDLINE-86245056; PubMed-2424612;
Alizon M., Wain-Hobson S., Montagnier L., Sonigo P.;
"Genetic variability of the AIDS virus: nucleotide sequence analysis of two isolates from African patients.";
                                                                                                                                                                                                                                                                                                                CHAIN
                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                  AIDS; Core protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HIV; K03454; GAG$ELI.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human immunodeficiency virus type 1 (ELI isolate) (HIV-1). Viruses; Retroid viruses; Retroviridae; Lentivirus.
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InterPro; IPR000071; Retrovir_p17.
InterPro; IPR001878; Znf_CCHC.
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                                                                       Local
    2 KARVLAEA 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FUNCTION: PERFÓRMS HIGHLY COMPLEX ORCHESTRATED TASKS DURING THE ASSEMBLY, BUDDING, MATURATION, AND INFECTION STAGES OF THE VIRA REPLICATION CYCLE. DURING VIRAL ASSEMBLY, THE PROTEINS FORM MEMBRANE ASSOCIATIONS AND SELF-ASSOCIATIONS THAT ULTIMATELY RESULT IN BUDDING OF AN IMMATURE VIRION FROM THE INFECTED CELL. GAG PRECURSORS ALSO FUNCTION DURING VIRAL ASSEMBLY TO SELECTIVE BIND AND PACKAGE TWO PLUS STRANDS OF GENOMIC RNA. PTM: THE P24 PROTEIN IS PHOSPHORYLATED.
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CORE PROTEIN P17 (
CORE PROTEIN P24 (
CORE PROTEIN P7 ()
CORE PROTEIN P1 ()
CORE PROTEIN P1.
CORE PROTEIN P1.
                                                                                                                                                                                            CORE PROTE
CCHC-TYPE
                                                                       Score 35;
Pred. No.
                                                                                                                                                                     MYRISTATE
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                                                                                                                                               8A1785A59EAED08D CRC64;
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KARVLAEA 365

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ACC P0459
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PÉAM; PF00540; Gag_D17; 1.

PÉAM; PP00607; Gag_D24; 1.

PEAM; PP0060939; C2HCZNFINGER.

PRINTS; PR00939; C2HCZNFINGER.

PRINTS; PR00234; HTV1MATRIX.

SMART; SM00343; ZPF_CZHC; 2.

PROSITE; PS50158; ZFF_CCHC; 2.
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-I- FUNCTION: PERFORMS HIGHLY COMPLEX ORCHESTRATED TASKS DURING THE ASSEMBLY, BUDDING, MATURATION, AND INFECTION STAGES OF THE VIRAL ASSEMBLY, THE PROTEINS FORM MEDICATION CYCLE. DURING VIRAL ASSEMBLY, THE PROTEINS FORM MEMBRANE ASSOCIATIONS AND SELF-ASSOCIATIONS THAT ULTIMATELY RESULT IN BUDDING OF AN IMMATURE VIRTON FROM THE INFECTED CELL. GAG PRECURSORS ALSO FUNCTION DURING VIRAL ASSEMBLY TO SELECTIVELY BIND AND PACKAGE TWO PLUS STRANDS OF GENOMIC RNA.

-I- PTM: THE P24 PROTEIN IS PHOSPHORYLATED.

-I- SIMILARITY: CONTAINS 2 CCHC-TYPE ZINC FINGERS.
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P04591;
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HSSP; P05888; 1AAF.
HIV; K03455; GAG$HXB2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ratner L., Fisher A., Jagodzinski L.L., Mitsuya H., Gallo R.C., Wong-Staal F.; "Complete nucleotide sequences of functional clones
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13-AUG-1987 (Rel. 05, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
GAG polyprotein (Contains: Core proteins P17, P24, P2, P7, P1, P6).
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Zinc-finger;
                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR000071; InterPro; IPR001878;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           entities requires a license agreement (See http://www.isb-sib.ch/announce/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human immunodeficiency virus type 1 (HXB2 isolate) (HIV-1).
Viruses; Retroid viruses; Retroviridae; Lentivirus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID-11706;
358 KARVLAEA 365
                                                 N
                          KARVLAEA 9
                                                                                              8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IPR000721;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     protein;
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                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Repeat.
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2nf_CCHC.
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CORE PROTEIN P17 (
CORE PROTEIN P24 (
CORE PROTEIN P2.
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CORE PROTEIN P1.)
                                                                                                                        Score 35;
Pred. No.
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774C384D6EACB108 CRC64;
                                                                                                                                                                                                                                                CCHC-TYPE 1.
CCHC-TYPE 2.
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RESULT
GAG_HV1
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Matches 8
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InterPro; IPR000071; Retrovir_p17.
InterPro; IPR001878; Znf_CCHC.
Pfam; PF00098; zf-CCHC; 2.
Pfam; PF00540; Gag_p17; 1.
Pfam; PF00540; Gag_p24; 1.
Pfam; PF00607; Gag_p28; 1.
PRINTS; PR00939; C2HCZNFINGER.
PRINTS; PR00939; C2HCZNFINGER.
PRINTS; SM00343; ZNF_C2HC; 2.
PRART; SM00343; ZNF_C2HC; 2.
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p12494;
01-OCT-1989 (Rel. 12, Create;
01-FEB-1994 (Rel. 28, Last a;
15-JUN-2002 (Rel. 41, Last a)
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AIDS Res. Hum. Retroviruses 5:411-419(1999).

AIDS Res. Hum. Retroviruses 5:411-419(1999).

FUNCTION: PERFORMS HIGHLY COMPLEX ORCHESTRATED TASKS DURING THE ASSEMBLY, BUDDING, MATURATION, AND INFECTION STAGES OF THE VIRAL REPLICATION CYCLE. DURING VIRAL ASSEMBLY, THE PROTEINS FORM MEMBRANE ASSOCIATIONS AND SELF-ASSOCIATIONS THAT ULTIMATELY RESULT IN BUDDING OF AN IMMATURE VIRION FROM THE INFECTED CELL. GAG PRECURSORS ALSO FUNCTION DURING VIRAL ASSEMBLY TO SELECTIVELY BIND AND PACKAGE TWO PLUS STRANDS OF GENOMIC RNA.

1- PTM: THE P24 PROTEIN IS PHOSPHORYLATED.

5-1- SIMILARITY: CONTAINS 2 CCHC-TYPE ZINC FINGERS.
                                                                                                                                                                                                                                                                                                                                                                                     EMBL; M21137; AAB03522.1; -. HSSP; P05888; IAAF. HIV; M21137; GAGSJH3.
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                                                                                                                                                                                        CHAIN
                                                                                                                                                                                                                 AIDS; Core protein;
Zinc-finger; Repeat.
                                                                                                                                                                                                                                          SMART; SM00343; ZnF_C2HC; PROSITE; PS50158; ZF_CCHC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human immunodeficiency virus type 1 (JH3 isolate) (HIV-1).
Viruses; Retroid viruses; Retroviridae; Lentivirus.
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                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                              or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Komiyama N., Hattori N., Inoue J., Sakuma 9
"Nucleotide sequences of gag and env genes"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-89352108; PubMed-2669897;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ween the Swiss Institute of Bioinformatics and the European Bioinformatics Institute. There are no rest by non-profit institutions as long as its content
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SWISS-PROT entry is copyright. It is produced through a collaboration sen the Swiss Institute of Bioinformatics and the EMBL outstation -
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    41, Last annotation update)
    [Contains: Core proteins P17,

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CORE PROTEIN P2.
CORE PROTEIN P7 (NUCLEOCAPS)
CORE PROTEIN P1.
CORE PROTEIN P6.
CCHC-TYPE 1.
CCHC-TYPE 2.
MYRISTATE (BY SIMILARITY).
MY: 52E2812D4424AEE9 CRC64;
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              Score 35; pred. No.
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1 Japanese is
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A Shaw G.M., Kong L.I., Weiss S.H., Waters D., Gallo R.C., Blattner W.;
T "Viral variability and serum antibody response in a laboratory worker
infected with HIV type 1 (HTLV type IIIB).";
LAIDS Res. Hum. Retroviruses 10:1143-1155(1994).
C -!- FUNCTION: PERFORMS HIGHLY COMPLEX ORCHESTRATED TASKS DURING THE
ASSEMBLY, BUDDING, MATURATION, AND INFECTION STAGES OF THE VIRAL
C REPLICATION CYCLE. DURING VIRAL ASSEMBLY, THE PROTEINS FORM
MEDICATION CYCLE. DURING VIRAL ASSEMBLY, THE PROTEINS FORM
C MEMBRANE ASSOCIATIONS AND SELF-ASSOCIATIONS THAT ULTIMATELY
RESULT IN BUDDING OF AN IMMATURE VIRION FROM THE INFECTED CELL.
C GAG PRECURSORS ALSO FUNCTION DURING VIRAL ASSEMBLY TO SELECTIVELY
C GAG PRECURSORS ALSO FUNCTION DURING VIRAL ASSEMBLY TO SELECTIVELY
C GAG PRECURSORS ALSO FUNCTION DURING VIRAL ASSEMBLY TO SELECTIVELY
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C GAG PRECURSORS ALSO FUNCTION DURING VIRAL ASSEMBLY TO SELECTIVELY
C GAG PRECURSORS ALSO FUNCTION DURING VIRAL ASSEMBLY TO SELECTIVELY
C BIND AND PACKAGE TWO PLUS STRANDS OF GENOMIC RNA.
C -1- SIMILARITY: CONTAINS 2 CCHC-TYPE ZIMC FINGERS.
                                                                                                                Matches
                                                                                                                                        Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF00098; zf-CCHC; 2.
Pfam; PF00540; Gag_P17; 1.
Pfam; PF00607; Gag_P24; 1.
PRINTS; PR00939; C2HCXNFINGER.
PRINTS; PR00234; HYVIMATRIX.
SMART; SM00343; ZnF_C2HC; 2.
PROSITE; PS50158; ZF_CCHC; 2.
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_HV1LW
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ZN_FING
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15-JUL-1998 (Rel. 36, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
GAG polyprotein (Contains: Core proteins P17,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR000721; Gag_p24.
InterPro; IPR000071; Retrov1r
InterPro; IPR001878; Znf_CCHC
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Viruses; Retroid viruses; Retroviridae; Lentivirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q70622;
15-JUL-1998
                                                                                                                                                                                                                              SEQUENCE
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                                                        2 KARVLAEA 9
KARVLAEA 365
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                                                                                                          8; Conserv
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CORE PROTEIN P6 (
CORE PROTEIN P1 (
CORE P1 
                                                                                                                                        Score 35;
Pred. No.
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AA2F683546EDC0A9 CRC64;
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                                                                                                             Indels
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GAG_HYUN5
ID GAG_HYUN5
ID GAG_HYUN5
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ID GAG, HUMAN
OX NCHL,
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RESULT 14
GAG_HV1Y2
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Pfam; PF00540; Gag_pl7; 1.
Pfam; PF00607; Gag_p24; 1.
PRINTS; PR00939; C2HCZNFINGER.
PRINTS; PR00234; HIVIMATRIX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; M19921; AAA44987.1; -. HSSP; P05888; 1AAF. HIV; M19921; GAG$NL43.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. (CLONE PNL4-3).

Buckler C.E., Buckler-White A.J., Willey R.L., McCoy J.; Submitted (JUN-1988) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GAG polyprotein [Contains: Core proteins P17,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  P12493;
01-0CT-1989 (Rel. 12, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AIDS; Core protein;
Zinc-finger; Repeat
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InterPro; ipR000071; Retrovir_p17.
InterPro; ipR001878; Znf_CCHC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 movester and this statement is not removed. Usage by and for commercial requires a license agreement (See http://www.isb-sib.ch/announce/
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                                                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SMART; SM00343; ZnF_C2HC; PROSITE; PS50158; ZF_CCHC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Viruses; Retroid viruses; Retroviridae; Lentivirus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro;
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                                                                                                                        358 KARVLAEA 365
                                                                                                                                                       2 KARVLAEA
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STMILARITY: CONTAINS 2 CCHC. TYPE ZINC FINGERS.
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100.0%; F1
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CORE PROTEIN P1.
CORE PROTEIN P6.
CCHC-TYPE 1.
CCHC-TYPE 1.
CCHC-TYPE 2.
MYRISTATE (BY SIMILARITY).
WF. CBECC1302FE2C1E2 CRC64;
                                                                                                                                                                                                                                            Score 35;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BY SIMILARITY.

CORE PROTEIN P17 (MATRIX PROTEIN).

CORE PROTEIN P24 (CORE ANTIGEN).

CORE PROTEIN P2.
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GAG_HV1Y2

STANDARD;

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Best Local :
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InterPro; IPR000071; Retrovir_p17.
InterPro; IPR000878; Znf_CCHC.
Pfam; PF00098; Zf-CCHC; 2.
Pfam; PF000940; Gag_p17; 1.
Pfam; PF000540; Gag_p24; 1.
Pfam; PF000507; Gag_p24; 1.
Pfam; PF000343; Znf_CCHC; 2.
PR003343; HIVLMATRIX.
SMART; SM00343; Znf_CCHC; 2.
PR0051TE; PS50158; ZF_CCHC; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11)
SEQUENCE FROM N.A.
MEDLINE-93021387; Pubmed-1404605;
MED. """ H., Burgess C.J., Pric
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ZN_FING
LIPID
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                                                                                      SEQUENCE
                                                                                                                                                                                                AIDS; Core protein; 1
Zinc-finger; Repeat.
INIT_MET 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Complete nucleotide sequence, genome organization, and biological properties of human immunodeficiency virus type 1 in vivo: evidence for limited defectiveness and complementation.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Shaw G.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human immunodeficiency virus type 1 (YU-2 isolate) (HIV-1).
Viruses; Retroid viruses; Retroviridae; Lentivirus.
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01-JUN-1994 (Rel. 29, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
GAG polyprotein [Contains: Core proteins P17, P24, P2,
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358
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KARVLAEA
                    KARVLAEA 9
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P05888; 1AAF.
                                         Similarity 100.0%;
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CORE PROTEIN P24 (CC
CORE PROTEIN P2.
CORE PROTEIN P7.
CORE PROTEIN P7.
CORE PROTEIN P6.
CORE PROTEIN P6.
CCHC-TYPE 1.
CCHC-TYPE 2.
WYRISTATE (BY SIMILAW; 278E665F5405CD99.
                                           0
                                                    Score 35;
Pred. No.
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                                          Mismatches
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                                                                                    SIMILARITY).
5CD99 CRC64;
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RESULT

Search completed: March Job time: 5.27273 secs

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InterPro; IPR00071; Retrovir_p17.
InterPro; IPR00078; Znf_CCHC.
Pfam; PF00098; Zf-CCHC; 2.
Pfam; PF00540; Gag_p17; 1.
Pfam; PF005607; Gag_p24; 1.
Pfam; PF0060939; C2HCZNFINGER.
PRINTS; PR00934; HIVLMATRIX.
SMART; SM00344; HIVLMATRIX.
SMART; SM00343; ZnF_C2HC; 2.
PROSITE; PS50158; ZF_CCHC; 2.
                                                                                                     LIPID
SEQUENCE
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P12495;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-OCT-1989 (Rel. 12, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
GAG polyprotein [Contains: Core proteins P17,
                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; M22639; AAA45365.1; -. HSSP; P05888; IAAF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboratic between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on it use by non-profit institutions as long as its content is in no was
                                                                                                                                                                                                                           CHAIN
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INIT_MET 0
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Viruses; Retroid viruses; Retroviridae; Lentivirus.
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359
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SIMILARITY: CONTAINS 2 CCHC-TYPE ZINC FINGERS.
               KARVLAEA
KARVLAEA
                                                 8; Conserv
                                                                                                                                                                                                                                                                protein;
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CORE PROTEIN P24 (CORE ANTI)
CORE PROTEIN P2 (NUCLEOCAPS
CORE PROTEIN P1 (NUCLEOCAPS
CORE PROTEIN P6.
CCHC-TYPE 1.
CCHC-TYPE 2.
MYRISTATE (BY SIMILARITY).
M; B27C2609A992FB2A CRC64;
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                                                               Score 35;
Pred. No.
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//gn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*
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US-09-984-245-173
US-09-989-735-373
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US-09-957-485-4

Sequence 4, Application US/09957485

Patent No. US20020143165A1

GENERAL INFORMATION:
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PRIOR APPLICATION NUMBER: 60/124,270
PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 1556
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 804
LENOTH: 361
TYPE: PRI
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US-09-987-021-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; ORGANISM: Homo sapiens US-09-925-299-804
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: PatentIn Ver. SEQ ID NO 4
                                                                                                                                                                                                                                                                                                                Matches
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Best Local
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Best Local Similarity 70.0%;
Matches 7; Conservative
                  APPLICANT: Human Genome Sciences, Inc. et al. TITLE OF INVENTION: Brain-Associated Inhibitor TITLE OF INVENTION: Activator FILE REFERENCE: PF336P1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: Brain-Associated Inhibitor of Tissue-Type Plasminogen Activator FILE REFERENCE: PF356P2 CURRENT APPLICATION NUMBER: US/09/987,021 CURRENT FILING DATE: 2001-11-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR FILING DATE: 1996-
NUMBER OF SEQ ID NOS: 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: 08/948,997 PRIOR FILING DATE: 1997-10-10 PRIOR APPLICATION NUMBER: 60/028,117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: 09/722,292
PRIOR FILING DATE: 2000-11-28
PRIOR APPLICATION NUMBER: 60/247,971
PRIOR FILING DATE: 2000-11-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: 09/521,664
PRIOR FILING DATE: 2000-03-08
PRIOR APPLICATION NUMBER: 09/348,817
PRIOR FILING DATE: 1999-07-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: 09/957,485
PRIOR FILING DATE: 2001-09-21
                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
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                                                                                                                                                                                                                                   ADFSSFSDQE 336
APPLICATION NUMBER: US/09/957,485
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7; Conserv
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Pred. No.
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                                                    of Tissue-Type Plasminogen
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Sequence 75, Application US/10101464A

Publication No. US20030046728A1

GENERAL INFORMATION:
APPLICANT: Strabala, Timothy
APPLICANT: Nieuwenhuizen, Nicolaas
APPLICANT: Higgins, Colleen M.
TITLE OF INVENTION: Compositions Isolated from the Model of the 
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US-10-101-464A-75
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APPLICANT: Meyers, Rachel A.

APPLICANT: Meyers, Rachel A.

TITLE OF INVENTION: 26443 and 46873, NOVEL HUMAN

TITLE OF INVENTION: ASPARAGINASE FAMILY MEMBERS AND USES THEREFOR

FILE REFERENCE: 10448-029001

CURRENT APPLICATION NUMBER: US/09/816,664

CURRENT FILING DATE: 2001-03-23

PRIOR APPLICATION NUMBER: US 60/191,973

PRIOR APPLICATION NUMBER: US 60/191,973

PRIOR FILING DATE: 2000-03-24

NUMBER OF SEO ID NOS: 9

SOFTWARE: FASTSEQ for Windows Version 4.0

SEQ ID NO 7

FENCH. 378
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Best Local Similarity 70.0
Conservative
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CURRENT APPLICATION NUMBER: US/10/101,464A CURRENT FILING DATE: 2002-03-18 PRIOR APPLICATION NUMBER: 09/704,302 PRIOR FILING DATE: 2000-11-01 PRIOR APPLICATION NUMBER: 09/228,986 PRIOR APPLICATION NUMBER: 09/228,986 PRIOR FILING DATE: 1999-01-12
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PRIOR APPLICATION NUMBER: US 09/521,664
PRIOR FILING DATE: 2000-03-08
PRIOR APPLICATION NUMBER: US 60/123,704
PRIOR FILING DATE: 1999-03-10
NUMBER OF SEQ ID NOS: 21
SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 378
TYPE: PRT
ORGANISM: Artificial Sequence
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TYPE: PRT
ORGANISM: Bos taurus
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hes 6; Conserv
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Pred. No.
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Modification of
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; NUMBER OF SEQ ID NOS: 989
; SOFTWARE: FastSEQ for Windows V
; SEQ ID NO 75
; LENGTH: 659
; TYPE: PRT
; ORGANISM: Eucalyptus grandis
US-10-101-464A-75
                                 CURRENT APPLICATION NUMBER: US/09/998,598
CURRENT FILING DATE: 2001-11-16
NUMBER OF SEQ ID NOS: 2606
SOFTWARE: Corixa Invention Disclosure Database
SEQ ID NO 2593
LENCTH: 1331
TYPE: PRT
ORGANISM: Homo sapiens
US-09-998-598-2593
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Best Local Similarity
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Best Local Similarity
7; Conserve
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CURRENT FILING DATE: 2001-06-06
NUMBER OF SEQ ID NOS: 353
SOFTWARE: FASTSEQ FOR WINDOWS Version 3.0
'SEQ ID NO 347
LENGTH: 1531
TYPE: PRT
                                                                                                                                                                                              Sequence 2593, Application US/09998598
Patent NO. US20020150922A1
GENERAL INFORMATION:
APPLICANT: Stolk, John A.
APPLICANT: Xu, Jiangchun
APPLICANT: Chenault, Ruth A.
APPLICANT: Meagher, Madelein Joy
APPLICANT: Meagher, Madelein Joy
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF COLON CANCER
FILE REFERENCE: 210121.561
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 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR OVARIAN TITLE OF INVENTION: CANCER THERAPY AND DIAGNOSIS FILE REFERENCE: 210121.466C3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Benson, Darin R.
APPLICANT: Lodes, Michael J.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: King, Gordon E.
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 64.78;
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Pred. No.
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 Score 33;
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 DB 10;
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Length 1531;
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                                                       ; FEATURE:
; NAME/KEY: SIGNAL;
LOCATION: -34..-1
US-09-731-872-352
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                                                                                                                                                                           SOFTWARE: Patent.pm
SEQ ID NO 352
LENGTH: 206
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Best Local
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LENGTH: 314
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 352,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Patent No. US20020102604A1 GENERAL INFORMATION:
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Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: BUILINGAME, RICHARD P.
TITLE OF INVENTION: "VITAMIN C PRODUCTION IN MICROORGANISMS AND PLANTS"
FILE REFERENCE: 3161-24
CURRENT APPLICATION NUMBER: US/09/318,271A
CURRENT FILING DATE: 1999-05-25
EARLIER APPLICATION NUMBER: 60/125,073
EARLIER FILING DATE: 1999-03-17
EARLIER FILING DATE: 1999-03-17
EARLIER FILING DATE: 1999-03-18
EARLIER APPLICATION NUMBER: 60/125,054
EARLIER APPLICATION NUMBER: 60/125,054
EARLIER FILING DATE: 1999-03-18
EARLIER FILING DATE: 1999-03-18
EARLIER FILING DATE: 1999-03-18
EARLIER FILING DATE: 1999-03-18
EARLIER FILING DATE: 1998-06-08
NUMBER OF SEQ ID NOS: 15
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Berry, Alan
APPLICANT: Running, Jeffrey A
APPLICANT: Severson, David K.
                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: US 60/169,629
PRIOR FILING DATE: 1999-12-08
PRIOR APPLICATION NUMBER: US 60/187,470
PRIOR FILING DATE: 2000-03-06
                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/09/731,872
CURRENT FILING DATE: 2000-12-07
                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Jobert, Severin
TITLE OF INVENTION: FULL-LENGTH HUMAN CDNAS ENCODING POTENTIALLY SECRETED PROTEINS
FILE REFERENCE: 78.US3.REG
                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Bougueleret, Lydie APPLICANT: Jobert, Severin
                                                                                                                                                                                                                                       NUMBER OF SEQ ID NOS: 482
                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Dumas Milne Edwards, Jean Baptiste
                                                                                                                              ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
                                                                                                                                                             TYPE: PRT
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5. US20020012979A1
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60.8%;
87.5%;
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0; Mismatches
Score
Pred.
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82;
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                  Length 206;
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GENERAL INFORMATION
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Patent No. US20020165374A1
PRIOR APPLICATION NUMBER: US 60/060,862
PRIOR FILING DATE: 1997-10-02
PRIOR FILING DATE: 397-10-02
NUMBER OF SEQ ID NOS: 343
SOFTWARE: Patentin Ver. 2.0
BEO ID NO 172
LENGTH: 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: 09/154,707 PRIOR FILING DATE: 1998-09-17
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CURRENT FILING DATE: 2001-10-29
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TITLE OF INVENTION: 87 Human Secreted Proteins
                                                                                                                                                                                                                                                                                                                                                                                                     OR APPLICATION NUMBER: US 60/048,186
OR FILING DATE: 1997-05-30
OR APPLICATION NUMBER: US 60/048,069
OR APPLICATION NUMBER: US 60/048,095
OR APPLICATION NUMBER: US 60/048,095
OR FILING DATE: 1997-05-30
OR APPLICATION NUMBER: US 60/048,131
OR APPLICATION NUMBER: US 60/048,131
OR FILING DATE: 1997-05-30
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FILING DATE: 1997-05-30
APPLICATION NUMBER: US 60/050,937
FILING DATE: 1997-05-30
APPLICATION NUMBER: US 60/048,187
FILING DATE: 1997-05-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 1997-03-21
APPLICATION NUMBER: US 60/048,094
FILING DATE: 1997-05-30
APPLICATION NUMBER: US 60/048,350
APPLICATION NUMBER: US 60/048,350
FILING DATE: 1997-05-30
                                                                                                                       APPLICATION NUMBER: US 60/054,804 FILING DATE: 1997-08-05 APPLICATION NUMBER: US 60/056,370 FILING DATE: 1997-08-19
                                                                                                                                                                                                  APPLICATION NUMBER: US 60/048,351
FILING DATE: 1997-05-30
APPLICATION NUMBER: US 60/048,154
FILING DATE: 1997-05-30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US 60/048,352 FILING DATE: 1997-05-30
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                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US 60/048,160 FILING DATE: 1997-05-30
                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US 60/048,355 FILING DATE: 1997-05-30
                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US 60/048,096 FILING DATE: 1997-05-30
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US-09-992-598-373
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                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILLING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/065186
PRIOR FILLING DATE: 1997-11-12
PRIOR APPLICATION NUMBER: 60/065311
PRIOR APPLICATION NUMBER: 60/066770
PRIOR FILING DATE: 1997-11-24
PRIOR FILING DATE: 1997-11-24
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PRIOR FILING DATE: 1998-02-25
PRIOR APPLICATION NUMBER: 60/078910
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CURRENT APPLICATION NUMBER: US/09/992,598
CURRENT FILING DATE: 2001-11-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR FILING DATE: 1997-06-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Acids Encoding the Same
                                                                                                                     PRIOR APPLICATION NUMBER: 60/1 PRIOR FILING DATE: 1998-05-28
                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: 60/083322 PRIOR FILING DATE: 1998-04-28
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                                                                             PRIOR FILING DATE: 1998-06-02
                                                                                              PRIOR APPLICATION NUMBER: 60/087607
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nes 7; Conserv
                                     APPLICATION NUMBER: 60/
FILING DATE: 1998-06-02
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Baker, Kevin P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Stewart
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Kljavin, Ivar J.
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Gerritsen, Mary E.
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Stewart, Timothy A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Paoni, Nicholas F.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Napier, Mary A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Goddard, Audrey
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DATE:
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                  NUMBER: 60/087759
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87.5%;
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Pred. No.
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PRIOR FILING DATE: 1998-06-17 APPLICATION NUMBER: 60/0 FILING DATE: 1998-06-18 APPLICATION NUMBER: 60/0 APPLICATION NUMBER: 60/ FILING DATE: 1998-06-17 APPLICATION NUMBER: 60/ FILING DATE: 1998-06-1 APPLICATION NUMBER: 60 FILING DATE: 1998-06-1 APPLICATION NUMBER: 60 FILING DATE: 1998-06-1 APPLICATION NUMBER: APPLICATION NUMBER: 60/0 APPLICATION NUMBER: 60/0 FILING DATE: 1998-06-10 APPLICATION NUMBER: 60/0 FILING DATE: 1998-06-10 APPLICATION NUMBER: 60/ APPLICATION NUMBER: 60/ FILING DATE: 1998-06-05 APPLICATION NUMBER: 60/ APPLICATION NUMBER: FILING DATE: 1998-0 APPLICATION NUMBER: 60/ FILING DATE: 1998-06-04 APPLICATION NUMBER: 60/ FILING DATE: 1998-06-04 FILING DATE: 1998-06-04 APPLICATION NUMBER: FILING DATE: APPLICATION NUMBER: FILING DATE: 1998-06-04 APPLICATION NUMBER: FILING DATE: APPLICATION NUMBER: FILING DATE: 1998-06-04 FILING DATE: 1998-0 APPLICATION NUMBER: APPLICATION NUMBER: 60/ FILING DATE: 1998-06-17 APPLICATION NUMBER: 60/ APPLICATION NUMBER: FILING DATE: 1998-00 APPLICATION NUMBER: FILING DATE: 1998-00 APPLICATION NUMBER: FILING DATE: 1998-06-1 APPLICATION NUMBER: 60/ FILING DATE: 1998-06-10 FILING DATE: APPLICATION NUMBER: FILING DATE: 1998-06-05 FILING DATE: 1998-00 APPLICATION NUMBER: APPLICATION NUMBER: FILING DATE: 1998-00 APPLICATION FILING DATE: APPLICATION NUMBER: FILING DATE: 1998-06-17 APPLICATION NUMBER: APPLICATION NUMBER: APPLICATION NUMBER: FILING DATE: APPLICATION NUMBER: FILING DATE: 1998-06-1 FILING DATE: FILING DATE: NUMBER: 60/0: 1998-06-18 NUMBER: 1998-06-1998-06-16 1998-06-10 1998-06-09 1998-06-05 1998-06-04 1998-06-04 1998-06-04 1998-06-1998-06-10 1998-06-1998-06-16 1998-06-16 60/087827 6-03 60/088217 60/089512 60/088734 60/088212 60/088202 60/088033 60/088029 60/088028 60/088026 60/088021 60/089907 60/088824 60/088810 60/088742 60/088655 60/088167 60/088326 60/088025 60/089947 80/089908 60/089801 60/089653 60/089600 60/089599 60/089598 60/089538 60/089532 60/089514 60/089440 60/089105 60/088876 60/088861 60/088858 60/088826 60/088738 60/088030

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OR FILING DATE: 1998-06-25
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OR APPLICATION NUMBER: 60/090696
OR FILING DATE: 1998-06-26
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OR FILING DATE: 1998-06-26 DR APPLICATION NUMBER: 60/090246
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DR APPLICATION NUMBER: 60/090254
DR FILING DATE: 1998-06-22
DR FILING DATE: 1998-06-23
DR APPLICATION NUMBER: 60/090349
DR APPLICATION NUMBER: 60/090355
DR APPLICATION NUMBER: 60/090355 DR FILING DATE: 1998-07-02

DR APPLICATION NUMBER: 60/091633

DR FILING DATE: 1998-07-02

DR APPLICATION NUMBER: 60/091978

DR FILING DATE: 1998-07-07

DR APPLICATION NUMBER: 60/091982

DR FILING DATE: 1998-07-07

DR FILING DATE: 1998-07-09

DR FILING DATE: 1998-07-09 FILING DATE: 1998-00 .
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Query Match 60.8%; Score 31; DB 9; Length 229; Best Local Similarity 87.5%; Pred. No. 93; Matches 7; Conservative 0; Mismatches 1; Indels 0;

Gaps

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CURRENT FILING DATE: 2001-11-20
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PRIOR APPLICATION NUMBER: 60/062250
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APPLICANT:
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APPLICATION NUMBER: 60/087827
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APPLICATION NUMBER: 60/088021
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Baker, Kevin P.
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Kljavin, Ivar J.
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Gerritsen, Mary E.
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R APPLICATION NUMBER: 60/089948
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DR APPLICATION NUMBER: 60/089952
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CURRENT FILING DATE: 2001-11-19
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/065186
PRIOR FILING DATE: 1997-11-12
PRIOR FILING DATE: 1997-11-12
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OR FILING DATE: 1998-03-20
OR APPLICATION NUMBER: 60/083322
OR FILING DATE: 1998-04-28
OR APPLICATION NUMBER: 60/084600
OR FILING DATE: 1998-05-07
OR APPLICATION NUMBER: 60/087106
OR FILING DATE: 1998-05-28
OR APPLICATION NUMBER: 60/087607
OR FILING DATE: 1998-06-02
OR APPLICATION NUMBER: 60/087609
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FILING DATE: 1998-06-04
APPLICATION NUMBER: 60/088026
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APPLICATION NUMBER: 60/088028
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FILING DATE: 1997-11-24
APPLICATION NUMBER: 60/075945
FILING DATE: 1998-02-25
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FILING DATE: 1998-06-03
APPLICATION NUMBER: 60/088021
FILING DATE: 1998-06-04
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FILING DATE: 1997-11-13
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Williams, P. Micke
Wood, William I.
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Stewart, Timothy A.
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APPLICATION NUMBER: 60/ FILING DATE: 1998-06-04

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OR APPLICATION NUMBER: 60/088326
OR FILING DATE: 1998-06-04
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OR APPLICATION NUMBER: 60/088167
OR APPLICATION NUMBER: 60/088202
OR FILING DATE: 1998-06-05
OR APPLICATION NUMBER: 60/088212
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OR APPLICATION NUMBER: 60/08874
OR APPLICATION NUMBER: 60/088810
OR APPLICATION NUMBER: 60/088824

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RESULT 15
US-09-990-444-373
: Sequence 373, Application US/09990444
: Publication No. US20020193300A1
: GENERAL INFORMATION:
: APPLICANT: Ashkenazi, Avi J.
: APPLICANT: Baker, Kevin P.
: APPLICANT: Botstein, David
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OR APPLICATION NUMBER: 60/089826
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R APPLICATION NUMBER: 60/08 R FILING DATE: 1998-06-19 R PELICATION NUMBER: 60/09 R APPLICATION NUMBER: 60/09 R FILING DATE: 1998-06-22 R FILING DATE: 1998-06-22

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PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/065186
PRIOR FILING DATE: 1997-11-12
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
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CURRENT FILING DATE: 2001-11-14
PRIOR APPLICATION NUMBER: 60/045787
PRIOR FILING DATE: 1997-06-16
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                            OR APPLICATION NUMBER: 60/088025
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OR APPLICATION NUMBER: 60/088028
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FILING DATE: 1997-11-24
APPLICATION NUMBER: 60/075945
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Gerber, Hanspeter
Gerritsen, Mary E.
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ALIGNMENTS

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US-08-365-103B-14
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                                                                                                                                                           REFERENCE/DOCKET NUMBER: UIRF
TELECOMMUNICATION INFORMATION:
TELEPHONE: (515) 288-367
TELEPAX: (515) 288-1338
INFORMATION: TOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 166 amino acids
                                Best Loc
Matches
                                                                 Query Match
                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/08/365
FILING DATE: 28-DEC-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Nebel, Heid1 S.
REGISTRATION NUMBER: 37,719
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Lynch, nature D.
APPLICANT: Nunez, Raphael D.
APPLICANT: Yodoi, Jungi
TITLE OF INVENTION: DAM Sequences for Soluble Froms
TITLE OF INVENTION: and Methods of Use for Same
TITLE OF SECUENCES: 14
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Zarley, McKee, Thomte, Voorhees & Sease
STREET: 801 Grand Ave. Suite 3200

CITY: Des Moines
STATE: Iowa
                                                                                                               TOPOLOGY: 11
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COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
                                               Local
                                                                                                                                                 TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY:
1 ADLSSFKSQEL 11
                                l Similarity
11; Conserv
                                                                                                                                               amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Application US/08365103B
                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              United States
                                                                                                                                  linear
                                                                                                               protein
                                                                                                                                                                                                                                                                                                                                                                                                                                               Floppy disk
                                              100.0%;
                                                                                                                                                                                                                                                                                                                                                               US/08/365,103B
                                  0;
                                                                                                                                                                                                                                                                 Uirf N5-24
                              Score 51; DB 1;
Pred. No. 0.011;
; Mismatches
                                                                  DB 1;
                                                                                                                                                                                                                                                                                                                                                                                               #1.25
                                  0;
                                                               Length 166;
                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  of CD23
                                  0;
                                  Gaps
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ADLSSFKSQEL

US-08-365-103B-12

atent No. 5766943 GENERAL INFORMATION:

Application US/08365103B

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                                                                                                                                                                                                                                                                                                                                                                            US-08-365-103B-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 100.0%; Score 51; Best Local Similarity 100.0%; Pred. No. Matches 11; Conservative 0; Mismatch
                                                                                                                                                                                                                                                                                              Patent No. 5766943
GENERAL INFORMATION:
APPLICANT: Lynch,
                                                                                                                                                                                                                                                                                                                                                      Sequence 10,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE: (515) 288-3367
TELEFAX: (515) 288-1338
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 167 amino acids
TYPE: amino acid
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/365,103B
FILING DATE: 28-DEC-1994
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0.
                                                                                                                                                                                                TITLE OF INVENTION: DNA Sequences for Soluble Froms of CD23 TITLE OF INVENTION: and Methods of Use for Same NUMBER OF SEQUENCES: 14
                                                                                                                                                                                                                                                  APPLICANT: Lynch, Richard G
APPLICANT: Nunez, Raphael D.
APPLICANT: yodol, Jungi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: Nebel, Heldi S.
REGISTRATION NUMBER: 37,719
REFERENCE/DOCKET NUMBER: Ulrf N5-24
TELECOMMUNICATION INFORMATION:
TELEPHONE: (515) 288-3667
                                                                                                                                                                            CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: DNA Sequences for Soluble Froms of CD23 TITLE OF INVENTION: and Methods of Use for Same
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Lynch, Richard G
APPLICANT: Nunez, Raphael D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STATE: IOWn
                                                                                                    CITY: Des Moines
STATE: Iowa
                                                                                                                                        STREET:
                                                              COUNTRY: UZIP: 50309
                                                                                                                                                                                                                                                                                                                                                                                                                                                       80 ADLSSFKSQEL 90
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                                                                                                                                                                                                                                                                                                                                      0, Application US/08365103B 5766943
                                                                                                  IOWB
                                                                                                                                        E: Zarley, McKee, Thomte, Voorhees & Sease
801 Grand Ave. Suite 3200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Yodoi, Jung:
                                                                              United States
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0.011;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0
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US-08-365-103B-8
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                                                                                                                           COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-POS
SOFTWARE: Patentin Release #1.0, Version #1.25
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/365,103B
FILING DATE: 28-DEC-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Nebel, Heidl S.
REGISTRATION NUMBER: 37,719
REFERENCE/DOCKET NUMBER: Uirf N5-24
TELECOMMUNICATION INFORMATION:
TELEPHONE: (515) 288-3667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 8, Applicati
Patent No. 5766943
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
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ATTORNEY/AGENT INFORMATION:
NAME: Nebel, Heidl S.
REGISTRATION NUMBER: 37,719
REFERENCE/DOCKET NUMBER: U1rf
TELECOMMUNICATION INFORMATION:
TELEPHONE: (515) 288-3667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: (515) 288-1338
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 320 amino acids
                                                                                          TELEFAX: (515) 288-1338 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
APPLICANT:
                                                                        SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: DNA Sequences for Soluble Froms of CD23
TITLE OF INVENTION: and Methods of Use for Same
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 320 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
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SOFTWARE: Patentin Rel
CURRENT APPLICATION DATA:
 MOLECULE TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: 801 Gran
CITY: Des Moines
STATE: Iowa
               TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/0 FILING DATE: 28-DEC-1994
                                                      LENGTH:
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                               : 321 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Application US/08365103B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nunez, Raphael D. Yodoi, Jungi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                E: Zarley, McKee, Thomte, Voorhees & Sease
801 Grand Ave. Suite 3200
                                                                                                                                                                                                                                                                                                                                                                                                                                       United States
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protein
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n Release #1.0, Version #1.25
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Query Match

100.0%; Score 51;

DB 1;

Length 321;

Best Local Similarity 100.0%; Matches 11; Conservative 0;

Pred. No. 0.022; ; Mismatches 0;

Indels

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Gaps

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US-09-348-817A-4
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GENERAL INFORMATION:
                                                                                           GENERAL INFORMATION:
APPLICANT: Hastings et al.
TITLE OF INVENTION: Brain-Associated Inhibitor of Tissue-Type Plasminogen
TITLE OF INVENTION: Activator
                                                                                                                                                                      Sequence 4, Application US/09348817A Patent No. 6191260
                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity
Matches 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
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FILE REFERENCE: PF336D1
CURRENT APPLICATION NUMBER: US/09/348,817A
CURRENT FILING DATE: 1999-07-08
PRIOR APPLICATION NUMBER: 08/948,997
PRIOR FILING DATE: 1997-10-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 402 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/08/948,997
FILING DATE: Oct-10-97
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: A. ANDERS BROOKES
REGISTRATION NUMBER: 36,373
REGERENCY/COURTE BROOKES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: BRAIN-ASSOCIATED INHIBITOR OF TITLE OF INVENTION: TISSUE-TYPE PLASMINOGEN ACTIVATOR NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: PF
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: HASTINGS, GREGG
                                                                                                                                                                                                                                                                                     327 ADFSSFSDQE 336
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid
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9410 KEY WEST AVENUE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COLEMAN, TIM
                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                             protein
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                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                      Length 402;
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RESULT 8

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17

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; LENGTH: 402
; TYPE: PRT
; ORGANISM: Bos taurus
US-09-348-817A-4
                                                                                                                ; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-261-825-2
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US-08-261-825-2
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                                                          Matches
                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/08/261,825
FILING DATE: 17-JUN-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: TUMARKIN, LISA A.
REGISTRATION NUMBER: P-38,347
REFERENCE/DOCKET NUMBER: PD3516
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: 60/
PRIOR FILING DATE: 1996-10-11
NUMBER OF SEQ ID NOS: 17
                                                                                                                                                                             TELEFAX: (619) 455-5110
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 174 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: Champi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET: LOS Angeles
CITY: LOS Angeles
STATE: Callfornia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: CLONED I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            327 ADFSSFSDQE 336
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                                                                        Local
                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                         TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE:
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                          2 DLSSFKSQEL 11
DLSAFMSQDI
                                                       Similarity
6; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Application US/08261825
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 E: Spensley Horn Jubas & Lubitz
1880 Century Park East, Suite 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Miller, James N.
Blanco, David R.
                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Lovett, Michael A. Haake, David A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Champion, Cheryl
                                                                                                                                                                                                                                           (619) 455-5100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      66.7%;
                                                                        64.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLONED Borrelia burgdorferi VIRULENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 34;
Pred. No.
                                                                       Score 33; DB 1; Length 174; Pred. No. 35;
                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                               Version #1.25
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RESULT 9
PCT-US95-07748A-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: (619) 455-5110
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 174 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/261,825
FILING DATE: 17-JUN-1994
ATTORNEY/ACENT INFORMATION:
NAME: TUMARKIN, LISA A.
REGISTRATION NUMBER: P-38,347
REFERENCE/DOCKET NUMBER: PD3516
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619),455-5100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                              NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
                                                                                                                                                                                                   TITLE OF INVENTION: CLONED E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: LOVELT, MICHAEL A.
APPLICANT: Haake, David A.
APPLICANT: Miller, James N.
APPLICANT: Blanco, bavid R.
TITLE OF INVENTION: CLONED Borrelia burgdorferi VIRULENCE
TITLE OF INVENTION: PROTEIN
                    COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
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                                                                                                                                                                                                                                                                                                                                                                   2 DLSSFKSQEL 11
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17 DLSAFMSQDI 26
                                                                        CITY: La Jolla
STATE: California
COUNTRY: USA
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                                                                                                                             STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
les 6; Conservat
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STATE: California
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   COMPUTER:
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                                                                                                                                                                                                                                                                             Application PC/TUS9507748A
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                                                                                                                             4225 Executive Square, Suite 1400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IB: Spensley Horn Jubas & Lubitz
1880 Century Park East, Suite 500
                                                                                                                                                                                                                    The Regents of the University of California VENTION: CLONED Borrelia burgdorferi VIRULENCE
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E: Floppy disk
IBM PC compatible
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Pred. No. 35;
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APPLICANT: Strabala, Timothy
APPLICANT: Nieuwenhuizen, Niels
TITLE OF INVENTION: Compositions Isolated from Plant Cells
TITLE OF INVENTION: And Their Use in the Modification of Plant Cell Signalling
FILE REFERENCE: 11000/1020
CURRENT APPLICATION NUMBER: US/09/228,986
CURRENT FILING DATE: 1999-01-12
NUMBER OF SEQ ID NOS: 130
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 75
LENCTH: 659
TYPE: PRT
ORGANISM: Eucalyptus grandis
US-09-228-986-75
                                                                                                                                                                                                      RESULT 11
US-08-889-402-1
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Best Local Similarity
"~+~hes 6; Conserv?
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                                                                              GENERAL INFORMATION:
TITLE OF INVENTION: NOVI
TITLE OF INVENTION: PRO'
NUMBER OF SEQUENCES: 7
COMPUTER READABLE FORM:
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                                                                                                                                                                Sequence 1, Application US/08889402
Patent No. 5811288
                                                                                                                                                                                                                                                                                                                                              Matches
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Best Local
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INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: HAILE, Ph.D., LISA A.
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 07.
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/07748A
FILING DATE: 16-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear MOLECULE TYPE: protein
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                            289 DVATEKHQEL 298
            COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0,
                                                                                                                                                                                                                                                                                                                                        Local Similarity
tes 6; Conserv
                                                              MEDIUM TYPE: Floppy disk
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                            Score 33; DB 4;
Pred. No. 1.4e+02;
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                Version #1.30 (EPO)
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                                                                                                                                      US-08-296-014A-4
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Best Local
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                                                                    Query Match
                                                                                                                                                                                                                                                           TELEFAX: (703) 205-805
TELEX: 248345
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 1019 amino aci
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: MULPHY, Jr., Gerald M.
REGISTRATION NUMBER: 26,977
REFERENCE/DOCKET NUMBER: 178:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOCTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
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                                                                                                                                                                     TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION: TELEPHONE: (703) 205-8000
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                                  Local
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CITY: Falls Church
STATE: Virginia
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mes 7; Conserv
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Similarity 54.96; Conservative
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8110 Gatehouse Road, Suite 500 East
                                                                                                                                                                                                                                                                 1019 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                          (703) 205-8050
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                                  62.7%;
54.5%;
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Pred. No.
Score 32; DB 1; Lo
Pred. No. 3.6e+02;
3; Mismatches 2;
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US-08-596-405-4
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US-08-877-620-4
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                                                                                                                                                          Patent No.
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Patent No. 5858706
                                                                                                                                                                       Sequence 4,
                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                        GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: (703) 205-80: TELEX: 248345 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
                                                               APPLICANT: Ding, Jea APPLICANT: HO, BOW TITLE OF INVENTION: TITLE OF INVENTION: TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Murphy, Jr., Gerald M.
REGISTRATION NUMBER: 28,977
REFERENCE/DOCKET NUMBER: 1783
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 205-8000
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Birch, Stewart, Ko
STREET: 8110 Gatehouse Road,
                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 1019 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
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TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              404 SDLNGIKSEEL 414
                                                                                                                                                                                                                                                    404 SDLNGIKSEEL 414
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: (703) 205-8050
                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                              Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER:
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SYSTEM: PC-DOS/MS-DOS
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                                                             The Cloned Factor C cDNA of the Singapore Horseshoe Crab, Carcinoscorpius rotundicauda and Purification of Factor C Proenzyme
                                                                                                                                                                                                                                                                                                                              62.7%;
54.5%;
                 Stewart, Kolasch
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Pred. No.
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   & Birch
500 East
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: Virginia RY: USA 22042

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Sequence 2, Application US/08296014A

Patent No. 5716834

GENERAL INFORMATION:
APPLICANT: Ding, Jeak Ling
APPLICANT: HO, Bow
TITLE OF INVENTION: Singapore Horseshoe Crab, Carcinoscorpius
TITLE OF INVENTION: rotundicauda and Purification of Factor C Proenzyme
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Birch, Stewart, Kolasch & Birch
STREET: 8110 Gatchouse Road, Suite 500 East
COTY: Falls Church
STATE: Virginia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           멍
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US-08-296-014A-2
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    Matches

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ATTORNEY/AGENT INFORMATION:
NAME: MUTPHY, Jr., Gerald M.
REGISTRATION NUMBER: 28,977
REFERENCE/DOCKET NUMBER: 1781-105P
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 205-8000
TELEPAX: (703) 205-8050
TELEPAX: (703) 205-8050
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 1019 amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: linear
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APPLICATION NUMBER: US/08/296,014A FILING DATE: CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MULTIPLY, Jr., Gerald M.
REGISTRATION NUMBER: 28,907
REGERENCE/DOCKET NUMBER: 1781-105P
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: ISM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/08/877,620
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/596,405
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les 6; Conserv
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54.5%;
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Pred. No. 3.6e+02;
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TELEFAX: (703) 205-8050
TELEX: 248345
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1083 amino acids
TYPE: amino acids
TYPE: amino acids
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-296-014A-2
Ouery Match
Best Local Similarity 54.5%; Pred. No. 3.8e+02;
Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps
Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps
OU 1 ADLSSFKSQEL 11
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Search completed: March 13, 2003, 18:53:51 Job time: 10.8 secs

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1 ADLSSFKSQEL 11
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O84483
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Q965R1
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Q982F6
Q00805
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Q19542
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                  Q9pr79 ureaplasma
Q982f6 rhizobium 1
Q0805 leishmania
Q9vub0 drosophila
Q9vub0 drosophila
Q9vvf8 drosophila
Q9vvf8 drosophila
Q9wm66 newcastle d
Q9fvy2 gry2a sativ
C084483 chlamydia t
C031711 bacillus su
                                                                                                                    Q9pjr6 chlamydia m
Q9f0b9 lactobacill
                                                                                                                                       P90872 caenorhabdi
Q19542 caenorhabdi
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 caenorhabdi
caenorhabdi
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ALIGNMENTS

P90872 PRELIMINARY; PRT; 305 AA.
P90872; P909723;
01-MAY-1997 (TrEMBLrel. 03, Created)
01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-JAN-1999 (TrEMBLrel. 09, Last annotation update)

Caenorhabditis elegans. Eukaryota; Metazoa; Nemat Rhabditidae; Peloderinae;

Nematoda; Chromadorea; Rhabditida; Rhabditoidea; rinae; Caenorhabditis.

SEQUENCE FROM N.A. NCBI_TaxID=6239; F39H2.3 protein.

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Wilson R., Ainscough R., Anderson K., Baynes C., Berks M.,
Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,
Craxton M., Dear S., Du, Connell M., Favello A., Fulton L.,
Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,
Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,
Lightning J., Lloyd C., Mcmurray A., Mortimore B., O'Callaghan M.,
Lightning J., Lloyd C., Mcmurray A., Mortimore B., O'Callaghan M.,
Parsons J., Percy C., Rifken L., Ropera A., Saunders D., Shownkeen R.,
Smaldon N., Smith A., Sonnhammer E., Staden R., Sulston J.,
Thomas K., Vaudin M., Vaughan K., Waterston R.,
Watson A., Weinstock L., Wilkinson Sproat J., Wohldman P.;
Kershaw J.;
Submitted (OCT-1996) to the EMBL/GenBank/DDBJ databases EMBL; Z81098; CAB03184.1; -.
EMBL; Z81080; CAB03184.1; JOINED.
                                                                      SEQUENCE FROM N.A.
                                                                                                    Nature 368:32-38(1994).
                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. MEDLINE=94150718; PubMed=7906398;
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RESULT 2
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ID Q19542;
AC Q19642;
AC F18C12.1 protein.
AC F18C12.1 protein.
AC F18C12.1 protein.
AC F18C12.1 protein.
AC ELKARYOCE; Metazoa; Nemato OC Rhabditidae; Peloderinae;
AC RABDITAXID-6239;
AC CELLATAXID-6239;
AC CELLATAXID-6239
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Best Local S
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Best Local S
Matches 8
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Q9PJR6;
01-OCT-2000
01-OCT-2000
01-JUN-2002
SEQUENCE FROM N.A.

STRAIN-MOPN / NIGG;

MEDLINE-20150255; PubMed-10684935;

Read T.D., Brunham R.C., Shen C., Gill S.R., Heidelberg White O., Hickey E.K., Peterson J., Utterback T., Berry Linher K., Weidman J., Khouri H., Craven B., Bowman C., Gwinn M., Nelson W., DeBoy R., Kolonay J., McClarty G., Eisen J., Fraser C.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL: Z81
EMBL: Z81
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                            1515
                                                                                                                                                                     Chlamydia muridarum.
Bacteria; Chlamydiales;
NCBI_TaxID=03560;
                                                                                                                                                                                                                                  DNA methyltransferase. TC0762.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Interpro; IPR004273; Dynein_heavy. Pfam; PF03028; Dynein_heavy; 1. SEQUENCE . 4131 AA; 469655 MW; F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Investigating biology.";
Science 282:2012-2018(1998).
EMBL; Z75536; CAA99830.1; -.
HSSP; P02632; ICB1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Caenorhabditis elegans.
Eukaryota; Metazoa; Nemato
Rhabditidae; Peloderinae;
NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Genome sequence of the nematode C.elegans:
investigating biology.":
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Z81098; CAB03089.1;
NCE 305 AA; 34360
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Caenorhabditis.
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, Last sequence up
, Last annotation
                                                                                                                                                                                                                                                                   Created)
Last sequence up
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                 g J.F.,
y K., Bass S.,
, Dodson R.,
, Salzberg S.L.,
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Best Local S
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Glass .... Cassell G.H.;
The complete so
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01-MAR-2001
01-MAR-2001
01-MAR-2001
                                                                                    SEQUENCE FROM N.A.
STRAIN-SEROVAR 3;
MEDILNE-20500219; PubMed-11048724;
Glass J.I., Lefkowitz E.J., Glass
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01-OCT-2000 (TrEMBLrel.
01-OCT-2000 (TrEMBLrel.
01-JUN-2002 (TrEMBLrel.
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                                                                                                                                                                                                                                                                                          Ureaplasma parvum (Ureaplasma urealyticum biotype
Bacteria; Firmicutes; Bacillus/Clostridium group;
                                                                                                                                                                                                                                                                                                                                                      PTA OR UU066
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Lamothe G.T.;

EPS cluster of Lactobacillus delbrueckii subsp.

Submitted (MAY-2000) to the EMBL/GenBank/DDBJ dai

EMBL; AF267127; AAG44713.1;
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Bacteria; Firmicutes; Bacillus/Clostridium
Lactobacillaceae; Lactobacillus.
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Pfam; PF01035; Methyltransf_1; 1.
TIGRFAMS; TIGR00589; ogt; 1.
PROSITE; PS00374; MGMT; UNKNOWN_1.
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                                                                                                                                                                                                                              Mycoplasmataceae; Ureaplasma.
NCBI_TaxID=134821;
                                                                                                                                                                                                                                                                                                                                                                                 Phosphotransacetylase.
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Nucleic Acids Res. 28:1397-1406(2000).
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7; Conserv
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173 AA;
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(TrEMBLrel. 16,
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                              sequence
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Last annotation update)
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Pred. No.
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                                                                                       J.S.,
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ostridium group; Lactobacillales;
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19;
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                                                                                       C.R.,
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                                                                                                                                                                                                                                                                                                Mollicutes;
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Best Local S
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EMBL; AE002106; AAF30471.1; -.
InterFro; IPR002505; PTA_PTB.
Pfam; PF01515; PTA_PTB; 1.
Complete proteome.
SEQUENCE 293 AA; 33369 MW;
                                                                                                                                                                                                                      P-glycoprotein E.
Leishmania tropica.
Eukaryota; Euglenozoa;
                                                                                                                                                                                                                                                                                                                                000805;
01-JUL-1997 (TrEMBLrel.
01-JUL-1997 (TrEMBLrel.
01-JUN-2002 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto Watanabe A., Idesawa K., Ishikawa A., Kawashima K., Kimura T., Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A., Mochizuki Y., Nakayama S., Nakazaki N., Shimpo S., Sugimoto M., Tabata S., Tanada M., Tabata S., T
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01-OCT-2001 (TrEMBLrel. 18, Created)
01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF00155; aminotran_1_2; 1. Plasmid; Complete proteome. SEQUENCE 379 AA; 40183 MW; 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Complete genome structure of Mesorhizoblum lot1."; DNA Res. 7:331-338(2000). EMBL; AP003015; BAB54503.1; -.
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MEDLINE=21082930; PubMed=11214968;
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                                         STRAIN-LRC-L39;
Lafuente E., Ca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   000805
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                                                                                                                 SEQUENCE FROM N.A.
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les 8; Conserv
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   E., Castanys S. (APR-1996) to
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                                                                                                                                                                                                                      Kinetoplastida;
   ., Gamarro F.;
the EMBL/GenBank/DDBJ databases
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21,
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                                                                                                                                                                                                                                                                                                                            Created)
Last sequence update)
Last annotation updat
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                                                                                                                                                                                                                      Trypanosomatidae; Leishmania
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RA Adams M.D. (Celniker S.E., Hilt R.A., Evans C.A., Gocayne J.D.,
RA Adams M.D. (Celniker S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfelifer B.D.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfelifer B.D.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Nelson C.R., Miklos G.L.G.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Henos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Gerry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Gerry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Gerry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Melson D.R., Murphy B., Murphy L., Murny D.M., Nelson K.A.,
RA Melson D.R., Welson K.A., Nixon K., Nusskern D.R., Packeb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K. Real Randers R.D. C., Scheeler F., Shen H.,
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CG17362 protein.
CG17362.
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PROSITE; PS00962; RIBOSOWAL_S2_1; UNKNOWN_1.
PROSITE; P500030; RRM_RNP_1; UNKNOWN_1.
ATP-binding.
SEQUENCE 1677 AA; 183007 MW; C49208921B71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Musc
Ephydroidea; Drosophilidae; Drosophila.
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Pfam; PF00005; ABC_tran; 2.
ProDom; PD00006; ABC_transportr;
PRODOM; SMART; SM00382; AAA; 1.
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InterPro; IPR001140; ABCtranprtrTM.
InterPro; IPR003439; ABC_transportr.
InterPro; IPR001865; Ribosomal_S2.
InterPro; IPR006504; RNA_rec_mot.
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14,
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Pred. No. 1.8e+02;
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Q9VVF8
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RA FitzHugh W., Calvo S., Engels R., Smirnov S., Atnoor D., Brown A.,
RA Allen N., Naylor J., Stange-Thomann N., DeArellano K., Johnson R.,
RA Allen N., Naylor J., Stange-Thomann N., DeArellano K., Johnson R.,
RA Linton L., McEwan P., McKernan K., Talamas J., Tirrell A., Ye W.,
RA Linton L., McEwan P., McKernan K., Talamas J., Tirrell A., Ye W.,
RA Linton L., McEwan P., McKernan K., Talamas J., Tirrell A., Ye W.,
RA Linton L., McEwan P., McKernan K., Talamas J., Tirrell A., Guss A.M.,
Redderich R., Liu J., Mukhopadhyay B., Reeve J.N., Smith K.,
RA Leigh J.A., Li W., Liu J., Mukhopadhyay B., Reeve J.N., Smith K.,
RA Leigh J.A., Unayam L.A., White O., White R.H., de Macario E.C.,
Rerry J.G., Jarrell K.F., Jing H., Macario A.J.L., Paulsen I.,
RA Springer T.A., Unayam L.A., White O., White R.H., de Macario E.C.,
Rerry J.G., Jarrell K.F., Jing H., Macario A.J.L., Paulsen I.,
Rerry J.G., Jarrell K.F., Jing H., Macario A.J.L., Lander E.,
Ra Pritchett M., Sowers K.R., Swanson R.V., Zinder S.H., Lander E.,
Ra Pritchett M., Sowers K.R., Swanson R.V., Zinder S.H., Lander E.,
Ra Pritchett M., Sowers K.R., Swanson R.V., Zinder S.H., Lander E.,
Ra Pritchett M., Birren B.,
The genome of Methanosarcina acetivorans reveals extensive metabolic and physiological diversity.;
Genome Res. 12:532-542(2002).
EMBL; AEO10726; AAM04083.1;
EMBL; AEO10726; AAM04083.1;
SOUENCE 467 AA; 51705 MW; FE440724FBB90EBF CRC64;
                                                                                                                                                                                                                                                                                                   Query Match
Best Local S
Matches 8
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    O9VVF8 PRELIMINARY;
O9VVF8;
01-MAY-2000 (TrEMBLrel. 1
01-MAY-2000 (TrEMBLrel. 1
01-MAY-2000 (TrEMBLrel. 1
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Q1-JUN-2002 (TrEMBLrel. 21, C

Q1-JUN-2002 (TrEMBLrel. 21, I

Q1-JUN-2002 (TrEMBLrel. 21, I

Hypothetical protein MA0641.

MA0641.
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"The genome sequence of Drosophila melanogaster.";
Science 287:2185-2195(2000).
EMBL: AR003536; AAR497799.1;
-FlyBase; FBgn0036393; CG17362.
SEQUENCE 183 AA; 19807 MW; BB6263A75679B9A2 CRC64;
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STRAIN-C2A / ATCC 35395 / DSM 2834;
MEDLINE-21929760; PubMed-11932238;
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Archaea; Euryarchaeota; Methanococci; Methanosarcinales; Methanosarcinaceae; Methanosarcina.
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les 8; Conserv
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72.7%;
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Smith H.O.,
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RA Adams M.D., Ceniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Adams M.D., Ceniker S.E., Holt R.A., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Holt R.A., Hoskins R.A., Galle R.F.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Ballew R.M., Basu A., Baxedala J., Bayrektaroglu L., Beasley E.M.,
RA Beson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Beson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Berkova D., Botchen M.R., Bouck J., Brokstein P., Brottler P.,
RA Borkova D., Botchen M.R., Bouck J., Brokstein P., Brottler P.,
RA Durbin K.J., Evangelista C.C., Ferrac C., Ferriera S., Fleischmann W.,
RA Cherry J.M., Cawley S., Dahlke C., Davnport L.B., Davles P.,
RA Durbin K.J., Evangelista C.C., Ferrac C., Ferriera S., Fleischmann W.,
RA Fosler C., Gabriellan A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Durbin K.J., Evangelista C.C., Ferrac C., Ferriera S., Fleischmann W.,
RA Horstin D., Houston K.A., Howland T.J., Hernandez J.R., Houck J.,
RA Hortin D., Houston K.A., Howland T.J., Wai M. H., Ibeywam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Marnison J.A., Ketchum K.A.,
RA Hortin D., Houston K.A., Howland T.J., Wai M. H., Ibeywam C.,
RA Hount S.M., May M., Murphy B., Murphy L., Muzny D.M., Lai Z.,
RA Hoult S.M., May M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Rainert K., Renington K.A., Nixon K., Nusskern D.R., Pacleb J.H.,
RA Hang E. S., Siden Klamos I., Simpson M., Skupski M.P., Smith T.,
RA Hang E. S., Fleit M., Saunders R.D.C., Scheeler F., Shen H.,
RA Hang E. S., Todor C., Turner R., Venter E., Hang A.H., Wang X.,
RA Hang E. S., Todor C., Turner R., Venter E., Hang A.H., Wang X.,
RA Hang S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Jeng X.H., Zhong W., Zhou X., Zhu X., Smith H.O.,
RA Jeng R., Shang R., Boots R.A., Rubhn G.M., Venter F., Shen H.,
Science 287.2185-2195(2000).

BOUENCE
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Bukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

Ephydroidea; Drosophilidae; Drosophila.

NCBI_TaxID=7227;
                                                                                                                    Q9WMH6;
01-NOV-1999 (TrEMBLrel.
01-NOV-1999 (TrEMBLrel.
01-MAR-2002 (TrEMBLrel.
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STRAIN-BERKELEY;
MEDLINE-20196006; PubMed-10731132;
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disease virus.
ssRNA negative-strand
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Pred. No.
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2.3e+02;
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Hypothetical
SEQUENCE 13
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SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
MEDLINE-20047980; PubMed-10580061;
MEDLINE-20047980; PubMed-10580061;
MeDatsion T., Buchholz U.J.,
                                            01-NOV-1998 (TrEMBLrel. 08, Created)
01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation updat
Hypothetical 14.5 kDa protein.
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Oryza sativa (Rice).
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Submitted (MAR-1999)
                                                                                                                    084483;
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  Methylated-DNA protein ADA OR CT477.
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NCBI_TaxID-11176;
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nes 7; Conserv
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Pro; IPR001016; Viral_RNA_pol_L.
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NCE 2204 AA; 248500 MW;
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137 AA; 1
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                                                                                                                                           PRELIMINARY;
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87.5%;
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RESULT 14
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                         RA Azevedo V., Bertero M.G., Bessieres P., Bolotin A.M., Alloni G.,
RA Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
RA Borriss R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,
RA Borriss R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,
RA Borriss R., Boursier L., Brans A., Errun M., Brignell S.C., Bron S.,
RA Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
RA Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
RA Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
RA Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
RA Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
RA Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
RA Fritz C., Fujita M., Fujita Y., Fume S., Galizzi A., Galleron N.,
RA Gliseppi G., Guy B.J., Haga K., Haiech J., Harwood C.R., Henaut A.,
RA Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,
RA Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,
RA Kobayashi Y., Koetter P., Koningstein G., Krogh S., Kumano M.,
RA Kobayashi Y., Koetter P., Koningstein G., Krogh S., Kumano M.,
RA Kobayashi Y., Koetter P., Koningstein G., Krogh S., Kumano M.,
RA Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M.,
RA Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,
RA Parro V., Pohl T.M., Portetelle B., Rapoport G., Rey M., Reynolds S.,
RA Rigger M., Rivolta C., Rocha E., Roche B., Rose M., Sadaie Y.,
RA Seton T., Scanlan E., Schleich S., Schroeter R., Scoffone F.,
Sekowska A., Seror S.J., Seror P., Stadaie Y.,
RA Takeuchi M., Tamakoshi A., Tanaka T., Terpstra P., Tognoni A.,
RA Takeuchi M., Tamakoshi A., Tanaka T., Terpstra P., Tognoni A.,
RA Viari A., Wambutt R., Wedler E., Wedler H., Weitzenedger T.,
RA Viari A., Wambutt R., Wedler E., Wedler H., Weitzenedger T.
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Best Local
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031711;
01-JAN-1998
01-JAN-1998
01-JUN-2002
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Science 282:754-759(1998).
EMBL; AE001321; AAC68077.1; -...
InterPro; IPR001497; Methyltransf_1.
Pfam; PF01035; Methyltransf_1; 1.
PROSITE; PS00374; MGWT; UNKNOWN_1.
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Stephens R.S., Kalman S., Lammel C.J., Fan J., Marathe R., Aravind
Mitchell W.P., Olinger L., Tatusov R.L., Zhao Q., Koonin E.V.,
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Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia.
Tosato V., Uchiyama S.,
Viari A., Wambutt R., We
Winters P., Wipat A., Ya
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacillus subtilis.
Bacteria; Firmicutes;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacillaceae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Davis R.W.;
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B (TrEMBLrel.
CTrEMBLrel.
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70.0%;
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05,
21,
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Last sequence update)
Last annotation update)
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                   Wedler H., Weitzenegger
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Henaut A.,
Tones L.,
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RESULT
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"csel5, cse60, and csk22 are new members of mother-cell-specific
RT sporulation regulons in Bacillus subtilis.";

J. Bacteriol. 179:389-398(1997).

C '1- SIMILARITY: BELONGS TO THE ATP-BINDING TRANSPORT PROTEIN FAMILY

C (ABC TRANSPORTERS).

REMBL: 299111, CAB13309.1; -.

REMBL: AF012285; AAC24910.1; -.

RICHETPRO; IPR003593; AAA_ATPase.

RINterPro; IPR003593; AAA_TATPAse.

RINterPro; IPR003439; ABC_transportr.

PFAm; PF00005; ABC_tran; 1.

R ProDom; PD000006; ABC_transportr; 1.

R PROSITE; PS000321; AAC; TRANSPORTER; 1.

R PROSITE; PS00221; ABC_TRANSPORTER; 1.

W ATP-binding: Transport; Complete proteome.

SEQUENCE 230 AA; 25272 MW; 59CD1FC50BD619DD CRC64;
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Best Local S
Matches 6
SEQUENCE FROM N.A.
STRAIN-BRISTOL N2;
Harmon G., Wohldmann P.;
"The sequence of C. elegant
                                                                                                                                                                                                                                                                                                                                                                        Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Chromadorea;
Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q965R1 PRELIMINARY; PRT; 588 AA.
Q965R1;
Q1-DEC-2001 (TrEMBLrel. 19, Created)
Q1-DEC-2001 (TrEMBLrel. 19, Last sequence update)
Q1-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Hypothetical protein Y97E10B.1.
                                                                                                                                     Science
                                                                                                                                                                                                                                         SEQUENCE FROM N.A. STRAIN-BRISTOL N2; MEDLINE-99069613;
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                                                                                                                                  "Genome sequence of the nematode C. elegans: a platform for investigating biology. The C. elegans Sequencing Consortium."; Science 282:2012-2018(1998).
                                                                                                                                                                                                                     None;
                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=6239;
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Hemila H., Palva A., Paulin L., Arvidson S., Palva I "Secretory S complex of Bacillus subtilis: sequence identity to pyruvate dehydrogenase.";
J. Bacteriol. 172:5052-5063(1990).
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Submitted (NOV-1997) to the EMBL/GenBank/DDBJ databases.
[3]
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STRAIN-168;
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  sequence of C. elegans cosmid Y97E10B.";
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                                                                                                                                                                                                                                           PubMed-9851916;
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Pred. No.
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Search completed: March 13, Job time: 25.8 secs
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Matches 7
                                                                                                                                       "Direct Submission.";
Submitted (JUL-2001) to the EMB:
EMBL; AC024881; AAK71410.1; -.
InterPro; IPR002875; DUF23.
Pfam; PF01697; DUF23; 1.
ProDom; PD004413; DUF23; 1.
SEQUENCE 588 AA; 68177 MW; (
                                                                                                                                                                                                                     SEQUENCE FROM N.A. STRAIN-BRISTOL N2; Waterston R.;
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                                              386 LSSFKDEEL 394
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                                                                                          Similarity 7; Conserv
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77.88;
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            2003, 18:51:56
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Pred. No.
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Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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     Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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31	31	31	31	31	31	31	31	31	31	31	31
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ALIGNMENTS

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	tissue-specific and IL-4-specific regulation of gene expression.":	of human Ec ensilon recentor II (Ec ensilon DII/CD23)	Yokota A., Kikutani H., Tanaka T., Sato R., Barsumian E.L.,	MEDLINE-89028672; PubMed-2972386;	ALTERNATIVE SPLICING.	:	386.810-	"Partial characterization of natural and recombinant number soluble	.U., Magnenat E., Aubonney N., Bonnetoy JY.;	Graber P., Pochon S., Regamey	-93038513; PubMed-1417742;	PARTIAL SEQUENCE, AND DISULFIDE BONDS.	[4]	receptor.";	d expression	r E., Frost H., Delespesse G.;	Inedin C. Hofstetter H. Sarfati M. Lovy C.A. Suter H. Alaimo D.	SEQUENCE FROM N.A.	[3]	Celi 47:657-665(1986).	Creatives of immental infinitely to econfine	Kishimoto T.;	Kaisho T., Uchibayashi N., Hardy R.R.,	S., Sato R., Barsumian E.L., Owaki	PubMed=28777	SEQUENCE FROM N.A.	Proc. Natl. Acad. Sci. U.S.A. 84:819-823(1987).	. 🗅	Lym	e T., Yodoi J.;	M., Kim C.W., H	MEDITINE - 8731 8255: Dibmed - 294 9326:	SECULENCE EBOW N P		rimates; Catarrhini; Hominidae;		HOMO sapiens (Human).) (FC-epsilon-RII) (CD23) (BLAST-2) (Immunoglobulin	epsilon FC receptor (Lymphocyte	-JUN-2002	(Rel. 06,	1988 (Rel. 06,		ECEZ HIMAN STANDARD: PRT: 321 AA.	E-7

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RT cell surface receptor CD23 and comparison of two independently

RT derived molecular models,";

RL PROTEIN SC1. 5:240-247(1996).

CC -1- FUNCTION: THIS RECEPTOR HAS ESSENTIAL ROLES IN THE REGULATION

CC OF IGE PRODUCTION AND IN THE DIFFERENTIATION OF B-CELLS (IT IS

CC A B-CELL-SPECIFIC ANTIGEN).

CC A SOLUBLE EXCRETED FORM.

CC A SOLUBLE EXCRETED FORM.

CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS; A (SHOWN HERE) AND B; ARE

CC PRODUCED BY ALTERNATIVE SPLICING.

CC -1- PTM: N- AND O-GLYCOSYLATED.

CC -1- PTM: N- AND O-GLYCOSYLATED.

CC INTROCELLANEOUS: THERE ARE TWO KINDS OF FC RECEPTORS ON LYMPHOCYTES

CC AND MONOCYTES.

CC AND MONOCYTES.

CC -1- SIMILARITY: CONTAINS 1 C-TYPE LECTIN FAMILY DOMAIN.

CC -1- DATABASE: NAME-PROW: NOTE-CD guide CD23 entry.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         [6]
3D-STRUCTURE MODELING OF LECTIN DOMAIN.
MEDLINE-94191542; PubMed-8142907;
MEDLINE-94191542; PubMed-8142907;
Padlan E.A., Helm B.A.;
Paddaing of the lectin homology domains of affinity Fc epsilon receptor (Fc epsilon R)
Receptor 3:325-341(1993).
                                                                                                                                                                                                                                                                                                                                             EMBL; M15059; AAA52434.1; -.
EMBL; M14766; AAA52435.1; -.
EMBL; X04772; CAA28465.1; -.
EMBL; M23562; AAA52433.1; -.
PIR; A26067; LNHUER.
PIR; A26164; A26164.
PIR; A26589; A26589.
PIR; A31924; A31924.
PIR; J10132; J10132.
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PROSITE; PSO0615; C_TYPE_LECTIN_2; 1.

IGE-bloding protein; Transmembrane; Glycoprotein; Receptor; B-cell; Repeat; Lectin; Signal-anchor; Alternative splicing; 3D-structure.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bajorath J., Aruffo A.;

"Structure-based modeling of the ligand binding d
"Structure-based modeling of the ligand binding d
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                                                                                                                                                                                                                                               Pfam; PF00059; lectin_c;
SMART; SM00034; CLECT; 1
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PDB; 1KJE; 03-APR-96,
Genew; HGNC:3612; FCER2.
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                                                                                EXTRACELLULAR (POTENTIAL)
C-TYPE LECTIN (LONG FORM)
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MEDLINE-98318631; PubMed-9653160;
Mao M., Fu G., Wu J.-S., Zhang Q.-H.
Mao M., Fu G., Wu J.-S., Zhang Q.-H.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mao M., Fu G., Wu J.-S., Zhang Q.-H., Zhou J., Kan L.-X., Huang Q.-H. He K.-L., Gu B.-W., Han Z.-G., Shen Y., Gu J., Yu Y.-P., Xu S.-H., Wang Y.-X., Chen S.-J., Chen Z.;

"Identification of genes expressed in human CD34(+) hematopoletic stem/progenitor cells by expressed sequence tags and efficient full-length cDNA cloning.";

Length cDNA cloning.";

Proc. Natl. Acad. Sci. U.S.A. 95:8175-8180(1998).
                                                                                                            InterPro; IPR005377; Vps26.
Pfam; PF03643; Vps26; 1.
Transport; Protein transpor
SEQUENCE 327 AA; 38024 M
                                                                                                                                                                                EMBL; AF054179; AAC39912.1; -. EMBL; AF175266; AAF89954.1; -. Genew; HGNC:12711; VPS26.
                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE-Colon;
Renfrew Haft C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VP26_HUMAN
075436;
                                                                                                                                                                     MIM; 605506;
                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=9606;
283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     118 ADLSSFKSQEL 128
                                                                    Local
                          2 DLSSFKSQEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 ADLSSFKSQEL
DRSSFKQQEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        77-2001 (Rel. 40, Created)
77-2001 (Rel. 40, Last sequence up
77-2001 (Rel. 40, Last annotation protein homolog.
                                                    Similarity
7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  269
321 AA;
                                                      Conservative
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292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11
                                                                                                            transport.
38024 MW;
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36468
                                                                    70.0%;
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1; Mis
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; F86708C0E6515B87 CRC64:
                                                                               Score 35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 51; DB 1;
Pred. No. 0.0046;
Mismatches (
                                                                                                              BD330759ABE9BFA9 CRC64;
                                                       Mismatches
                                                                    No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       on update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                327
                                                                                  DB 1;
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                                                      2,
                                                                                  Length 327;
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                                                       Indels
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RESULT 3
VSI4_TRYBB
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                                                                Query Match
Best Local
                                                    Matches
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01-MAY-1992 (Rel. 22, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Variant surface 91ycoprotein ILTAT 1.24 precursor (VSG).
Typanosoma brucei brucei.
                                                                                                                                DISULFID
DISULFID
CARBOHYD
                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                            InterPro; IPR001812; Trypan_glycop
Pfam; PF00913; Trypan_glycop; 1.
Glycoprotein; Antigen; Trypanosomia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Trypanosoma brucel.",
Nature 362:603-609(193).

-i- FUNCTION: VSG FORMS A COAT ON THE SURFACE OF
TYPANOSOME EVADES THE IMMUNE RESPONSE OF THE
A SERIES OF ANTIGENICALLY DISTINCT VSGS FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-93218763; Publ
Blum M.L., Down J.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Carrington M., Miller N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN-ISOlate MIAG 209;
MEDLINE-92046037; PubMed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
NCBI_TaxID=5702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VSI4_TRYBB
P26329;
                                                                                                                                                                         PROPEP
                                                                                                                                                                                                                                                                   PIR; S18449;
PDB; 2VSG; 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "A structural motif in the variant surface glycoproteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Variant specific glycoprotein of Trypanosoma brucei consists domains each having an independently conserved pattern of cyst
                                                                                                        SEQUENCE
                                                                                                                                                                                        CHAIN
                                                                                                                                                                                                     SIGNAL
                                                                                                                                                                                                               3D-structure.
                                                                                                                                                                                                                                                                                               EMBL; X56767; CAA40086.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Wiley D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            X-RAY CRYSTALLOGRAPHY (2.7 ANGSTROMS) OF 24-381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      residues
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                                                                                                                       LIPID
 56
                                                                                                                                                                                                                                                                                                                                                                                                                                   PI-PL
                                                                                                                                                                                                                                                                                                                                                                                                                                            SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor. A SOLUBLE FORM IS RELASED FROM RUPTURED CELLS BY THE ACTION OF
SDLNSFKTLEL 66
                         ADLSSFKSQEL 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Biol.
                                                  Similarity 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENES.
                                                                                                                                                                                                                                                                     25-NOV-98.
                                                    Conservative
                                                                                                                                                                                                                                                                                 S18449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       221:823-835(1991).
                                                                                                        AA
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491
514
162
204
443
491
55169
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ller N., Blum M.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PubMed-8464512;
                                                                68.68;
63.68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gurnett A.M.,
                                                                                                                                                                                                                            Trypanosomiasis; GPI-anchor; Membrane; Signal;
                                                                                                        ¥.
                                                               Score 35;
Pred. No.
                                                                                                      N-LINKED (GLCNAC. . .) (POTENTIAL).
GPI-ANCHOR (BY SIMILARITY).
E77395A9E9CFDC8E CRC64;
                                                                                                                                                                       VARIANT SURFACE GLYCOPROTEIN ILTAT 1.24 HYDROPHOBIC, REMOVED DURING MATURATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Carrington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Roditi I., Wiley
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15;
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RESULT 4
RPN3_YEAST

Conservative

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Best Loc
Matches
                                              Query Match
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Dietrich F.S., Mulligan J.T., Hennessey K.M., Allen E., Araujo R.,
Aviles E., Berno A., Brennan T., Carpenter J., Chen E., Cherry J.M.,
Chung E., Duncan M., Guzman E., Hartzell G., Hunicke-Smith S.,
Chung E., Duncan M., Guzman E., Hartzell G., Lew H., Lin D.,
Mosedale D., Nakahara K., Namp C., Lashkari D., Lew H., Lin D.,
Mosedale D., Nakahara K., Namath A., Norgren R., Oefner P., Oh C.,
Petel F.X., Roberts D., Sehl P., Schramm S., Shogren T., Smith V.,
Taylor P., Wei Y., Yelton M., Botstein D., Davis R.W.;
Submitted (DEC-1994) to the EMBL/GenBank/DDBJ databases.

-1- FUNCTION: Acts as a regulatory subunit of the 26S proteasome which the control of th
                                                                                                                                                                                                                                                                                                                                          the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Kominami K.-I., Okura N., Kawamura M., Demartino G.N., Slav Shimbara N., Chung C.H., Fujimuro M., Yokosawa H., Shimizu Tanahashi N., Tanaka K., Toh-E A.;
"Yeast counterparts of subunits S5a and p58 (S3) of the hum proteasome are encoded by two multicopy suppressors of ninimal. Biol. Cell 8:171-187(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-FEB-1995 (Rel. 31,
01-FEB-1996 (Rel. 33,
15-JUN-2002 (Rel. 41,
                                                                                                                                                                                                                                            EMBL; D78023; BAA11208.1;
EMBL; U18778; AAB64554.1;
SGD; S0000823; RPN3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 oxidase A2 gene, Dox-A2.";
Mol. Gen. Genet. 251:146-152(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kawamura M., Kominami K.-I., Takeuchi J., Toh-E A.;
"A multicopy suppressor of nini-l of the yeast Saccharomyces cerevisiae is a counterpart of the Drosophila melanogaster diphenol oxidase A. Jene Doy-A.".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                      SGD; S0000823; RPN3.
InterPro; IPR000717; PCI.
Pfam; PF01399; PCI; 1.
SMART; SM00088; PINT; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-97170075;
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MEDLINE-96242146;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RPN3_YEAST
                                                                                                                       CONFLICT
                                                                                                                                                    Proteasome
                    Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROTEASE, SUBUNIT: THE 26S PROTEASOME IS COMPOSED OF A CORE PROTEASE, AS THE 20S PROTEASOME, CAPPED AT ONE OR BOTH ENDS BY THE 19S REGULATORY COMPLEX (RC). THE RC IS COMPOSED OF AT LEAST 18 DIFFERENT SUBUNITS IN TWO SUBCOMPLEXES, THE BASE AND THE LII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SIMILARITY: BELONGS TO THE PROTEASOME SUBUNIT S3 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WHICH FORM THE PORTIONS PROXIMAL AND DISTAL CORE, RESPECTIVELY (BY SIMILARITY). DOMAIN: CONTAINS 1 PCI DOMAIN.
7; Conserv
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60422
                    70.0%;
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Last annotation updat
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                                                                                                  W.
Score 35; DB Pred. No. 16; 2; Mismatches
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D0DA1645B8DE958D
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                                                 Length 523;
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nin1-1.*;
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mizu Y.,
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RA SQUUROS J. Peat N. Hayles J. Baker S. Basham D., Bowman S.,

RA SQUUROS J. Peat N. Hayles J., Baker S. Basham D., Bowman S.,

RA Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,

RA Gentles S., Goble A., Hamin N., Harris D., Hidalgo J., Hodyson G.,

RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,

RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,

RA McOney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,

RA McOney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,

RA McOney P., Moule S., Wungall K., Murphy L., Niblett D., Odell C.,

RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,

RA Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,

RA Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,

RA Woodward J., Volckaert G., Aert R., Robben J., Grymonprez B.,

Wolfens I., Vanstreels E., Rieger M., Schaefer M., Whitehead S.,

RA Wolfens I., Vanstreels E., Rieger M., Schaefer M., Wheller Auer S.,

RA Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,

RA Eger P., Zimmermann W., Wedler H., Wambutt R., Purnelle B.,

Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,

RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,

RA Lucas M., Rochet M., Galllardin C., Tallada V.A., Garzon A., Thode G.,

RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,

RA Cerrutti L., Love T., McComble W. R., Paulsen I., Potashkin J.,

"The genome sequence of Schizosaccharomyces pombe.";

RI Shakovski G.V., Ussery D., Barrell B.G., Nurse P.;

"The Stmilarity: Contains 19 Heat Repeats."
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YAQ5_SCHPO
                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                        REPEAT
REPEAT
                                                                          REPEAT
REPEAT
                                                                                                                                                              EMBL; Z68198; CAA92385.1; Interpro; IPRO00357; HEAT_repeat. Pfam; PF02995; HEAT; 4. PROSITE; PS50077; HEAT_REPEAT; 4.
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01-FEB-1996 (Rel. 33, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Putative translational activator C18G6.05C (GCN1
SPAC18G6.05C.
                                                                                                                           Hypothetical
REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Schizosaccharomyces pombe (Fission yeast).
Eukaryotta; Fungi; Ascomycota; Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
Schizosaccharomyces.
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Q10105;
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| DLSSLRNQEL 68
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on regulation; Activator; Repeat. AT 1.
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Best Local
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16-OCT-2001 (Rel. 40, Last annotation update)
Plasminogen activator inhibitor-1 precursor (PAI-1) (Endothelial SERFLINEI OR PAII.
BOS TANIEN (PAII.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
MEDLINE-90067867; PubMed-2587231;
Mimuro J., Sawdey M., Hatlori M., Loskutoff D.J.;
"CDNA for bovine type 1 plasminogen activator inh.
Nucleic Acids Res. 17:8872-8872(1989).
                                                                                                                                                                                              -
                                                                                                                                                                                                                                 J. Cell Biol. 111:743-755(1990).

11- FUNCTION: THIS INHIBITOR ACTS AS "BAIT" FOR TISSUE PLASMINOGEN ACTIVATOR, URCKINASE, AND PROTEIN C. ITS RAPID INTERACTION WITTER MAY FUNCTION AS A MAJOR CONTROL POINT IN THE REGULATION OF
                                                                                                                                                                                                                                                                                                                      MEDLINE=90338128; PubMed=1696269;
Pepper M.S., Belin D., Montesano R., Orci L., Vassalli J.-D.;
"Transforming growth factor-beta 1 modulates basic fibroblast growth
factor-induced proteolytic and angiogenic properties of endothelial
cells in vitro.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 24-63.

MEDLINE-88329072; PubMed-3262060;

Katagiri K., Okada K., Hattori H., Ya

*Bovine endothelial cell plasminogen

Purification and heat activation. *;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           _BOVIN
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Bovidae; Bovinae; Bovidae; Bovidae; Bovinae; B
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Eukaryota; Metazoa;
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                                                                     FIBRINOLYSIS: PAIL IS INACTIVATED BY PROTECLYTIC ATTACK MISCELLANBOUS: (U-PA) AND THE TISSUE-TYPE (TPA), CLEAVING 369(R)-370(M) BOND.
MISCELLANEOUS: VASCULAR ENDOTHELIAL CELLS MAY BE THE PRINOF SYNTHESIS OF PLASMA PAI.
SIMILARITY: BELONGS TO THE SERPIN FAMILY.
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Pred. No. 93;
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en activator inhibitor.
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ACT_SITE
CARBOHYD
                                                                                                                                                                                                     MEDLINE-21235186; pubMed-11337471;

BOIOTIN A., Wincker P., Mauger S., Jaillon O., Malarme K.,

Weissenbach J., Ehrlich S.D., Sorokin A.;

"The complete genome sequence of the lactic acid bacterium Lactococcus
lactis ssp. lactis IL1403.";

Genome Res. 11:731-753(2001).

-I-FUNCTION: SbcCD cleaves DNA hairpin structures. These structures
can inhibit DNA replication and are intermediates in certain DNA
recombination reactions. The complex acts as a 3'->5' double
strand exonuclease that can open hairpins. It also has a 5'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SBCC_LACLA Q9CFZ0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15-JUN-2002
15-JUN-2002
15-JUN-2002
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SMART; SM00093; SERPIN; 1.
PROSITE; PS00284; SERPIN; 1.
                                           entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
                                                                      the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for con
                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                               STRAIN-IL1403;
                                                                                                                                                                                                                                                                                                                                                                                                                    Lactococcus lactis (subsp. lactis) (Streptococcus lactis).
Bacteria, Firmicutes; Lactobacillales; Streptococcaceae; Lactococcus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nuclease sbcCD subunit SBCC OR LL1321.
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InterPro; IPR000215; Serpin.
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PIR; S06745; S06745.
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              EMBL; AE006364; AAK05419.1; -
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   InterPro; IPR003439;
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                                                                                                                                                             single-strand endonuclease activity (By similarity). SUBUNIT: Heterodimer of sbcC and sbcD (By similarity). SIMILARITY: BELONGS TO THE SMC FAMILY. SBCC SUBFAMILY.
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X52906; CAA37094.1; -.
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(Rel. 41, Last sequence update)
(Rel. 41, Last annotation update)
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אור אס. 19;
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REACTIVE BOND.
N-LINKED (GLCNAC. . .) (POTENTIAL)
N-LINKED (GLCNAC. . .) (POTENTIAL)
N-LINKED (GLCNAC. . .) (POTENTIAL)
S -> L (IN REF. 2).
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-LINKED (GLCNAC. ..) (POTENTIAL)
-LINKED (GLCNAC. ..) (POTENTIAL)
-> L (IN REF. 2).
9053617333C7D130 CRC64;
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CARBOHYD
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01-OCT-1996 (Rel. 34, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation update)
Putative 125.2 kDa membrane glycoprotein in
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Eukaryota; Fungi; Ascomycota; Saccharomycotina; Sacciaromycetales; Saccharomycetaceae; Saccharomyces
                                             1056 DLSSFTSQD
                                                                                                                                      SEQUENCE
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                                                                                                                                                                                  CARBOHYD
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                                                                                                                                                                                                        Hypothetical TRANSMEM
                                                                                                                                                                                                                              InterPro; IPR002860; GH_BNR. Pfam; PF02012; BNR; 7.
                                                                                                                                                                                                                                                    EMBL; Z71680; CAA96347.1; -. SGD; S0005348; YNR065C.
                                                                                                                                                                                                                                                                                     entities requires a license agreement (Some send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
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P53751;
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SIMILARITY: BELONGS TO THE PEP1 FAMILY OF MEMBRANE GLYCOPROTEINS.
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7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nuclease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1046
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    34
223
268
468
543
                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                              1064
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ξ
                                                                                                                                                                                                                                                                                                                                                                                                              Floeth M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      41
239
432
505
867
                                                                                                                                                35
553
846
985
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATP-binding;
                                                                                                      66.7%;
77.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       66.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Exonuclease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           120199
                                                                                                                                      125199
                                                                                                                                                                                                       Transmembrane; Gl
7 POTENTIAL.
                                                                                                    .88;
                                                                                                                                   N-LINKED (GLCNAC. . .)
                                                                                       Pred. No. 58;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATP (POTENTIAL).
COILED COIL (POTENTIAL).
COILED COIL (POTENTIAL).
COILED COIL (POTENTIAL).
COILED COIL (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                             Fritz C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 34; DB pred. No. 54; 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          e; Endonuclease; DNA replication;
Coiled coil; Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8F70D00AC28F8691 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1116
                                                                                                                                                                                                                   Glycoprotein.
                                                                                                                                                                                                                                                                                                moved. Usage by and for commercial (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                Heuss-Neitzel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             update)
                                                                                                  58;
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                                                                                                               ٠.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BIO3-HXT17 intergenic
                                                                                          <u>ب</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 1046;
                                                                                                              Length 1116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Saccharomycetes
                                                                                                                                      CRC64;
                                                                                           Indels
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                                                                                                                                                                      (POTENTIAL).
(POTENTIAL).
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                                                                                                                                                           (POTENTIAL)
                                                                                                                                                (POTENTIAL)
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Matches 5
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P4997;
01-OCT-1996 (Rel
01-OCT-1996 (Rel
15-JUN-2002 (Rel
15-JUN-2002 (Rel
                                                                                                                                                                                                                                                                                                                                         ACT_SITE
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                   ACT_SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                the European Bloinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Leukotriene A-4 hydrolase (EC 3.3.2.6) (LTA-4 hydrolase) (Leukotriene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR001930; Ala_peptase.
InterPro; IPR000130; Zn_MTpeptdse.
Pfam; PF01433; Pept1dase_M1; 1.
PROSITE; PS00142; ZINC_PROTEASE; PARTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEROPS; M01.004; -. DictyDb; DD05072; lkha.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the Furnmenn Bioinformatics Tractitute There are no restrictions on the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Jho
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Dictyostelium discoideum (Slime mold).
Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium
                             Azotobacter
                                          Bacteria;
                                                       Azotobacter vinelandii.
                                                                                                                                                                                                                                                                                                                                                                       METAL
                                                                                                                                                                                                                                                                                                                                                                                                                         Metalloprotease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; U27538; AAA70101.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (JUL-1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A(4) hydrolase) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Multifunctional enzyme; Hydrolase; Leukotriene biosynthesis; Zinc;
                                                                                                                                                                                                                             196
                                                                                                                                                                                                                                                       N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           activity (By similarity).

CATALYTIC ACTIVITY: (7E,9E,112,142)-(5S,6S)-5,6-epoxyicosa-7,9,11.14-tetraenoate + H(2)O = (6Z,8E,10E,14Z)-(5S,12R)-5,12-dihydroxyicosa-6,8,10,14-tetraenoate.

COFACTOR: BINDS 1 ZINC ION (BY SIMILARITY).

PATHWAY: Leukotrienes biosynthesis: third step.

SUBCELLULAR LOCATION: Cytoplasmic (By similarity).

SIMILARITY: BELONGS TO PEPTIDASE FAMILY M1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         mitted (JUL-1995) to the EMBL/GenBank/DDBJ databases. FUNCTION: Hydrolyzes an epoxide moiety of leukotriene A4 to form leukotriene B4 (LTB-4). The enzyme also has some
                                                                                                                                                                                                                          DIKSFKTQQI 205
                                                                                                                                                                                                                                                       DLSSFKSQEL 11
                                                                                                                                                                                                                                                                                   Similarity
5; Conser
                                         Proteobacteria;
                                                                                                                                                                                                                                                                                                                                     2
4
23
90
316
                                                                            (Rel. 34, Created)
(Rel. 34, Last sequence update)
(Rel. 41, Last annotation updat
tion and repair protein recf.
                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                           <u>چ</u>
                                                                                                                                                        STANDARD;
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1
2
2
2
3
3
5
5
9
0
                                                                                                                                                                                                                                                                                                50.0%;
                                         gamma
                                                                                                                                                                                                                                                                                                                                           ME;
                                                                                                                                                                                                                                                                                             Score 33;
Pred. No.
                                                                                                                                                                                                                                                                                                                                     ZINC (CATALYTIC) (BY SIMILARITY).
BY SIMILARITY.
ZINC (CATALYTIC) (BY SIMILARITY).
ZINC (CATALYTIC) (BY SIMILARITY).
PROTON DONOR (POTENTIAL).
E8307415B991487A CRC64;
                                                                                                                                                        PRT;
                                         subdivision;
                                                                                   recF.
                                                                                                                                                        364
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                                                                                                                                                                                                                                                                                                              1;
                                         Pseudomonadaceae;
                                                                                                                                                                                                                                                                                                            Length 316;
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GGT_PSESP

GGT_PSESP

ID GGT_P

AC P3626

P3626

P01-JU

DT 01-JU

DT 01-JU

DT 01-NO

DE Gamma

GN GGT.

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Best Local S
Matches 7
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DOMAIN
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GGT_PSESP
P36267;
                      Biotechnol. Prog. 9:323-331(1993).

1 - CATALYTIC ACTIVITY: (5-L-glutamyl)-peptide + an amino acid peptide + 5-L-glutamyl-amino acid.

1 - PATHWAY: GGT PLAYS A KEY ROLE IN THE GAMMA-GLUTAMYL CYCLE, PATHWAY: FOR THE SYNTHESIS AND DEGRADATION OF GLUTATHIONE.

1 - SUBUNIT: THIS ENZYME CONSISTS OF TWO POLYPEPTIDE CHAINS, WINSTHESIZED IN PRECURSOR FORM FROM A SINGLE POLYPEPTIDE.

SYNTHESIZED IN PRECURSOR FORM FROM A SINGLE POLYPEPTIDE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                               Ishiye M., Yamashita M., Niwa "Molecular cloning of the gamu Pseudomonas strain.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
01-WOV-1997 (Rel. 35, Last annotation update)
Gamma-glutamyltranspeptidase precursor (EC 2.3.2.2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TIGRFAMS; TIGRO0611; recf; 1. PROSITE; PS00617; RECF_1; 1. PROSITE; PS00618; RECF_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; X86404; CAA60158.1; -.
InterPro; IPR001238; Recr.
InterPro; IPR003395; SMC_N.
Pfam; PF02463; SMC_N; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-96009876; PubMed-7557415;
Badran H., Venkatesh T.V., Kunnimalaiyaan M., Sharma N., Das H.
Molecular characterization of the Azotobacter vinelandii recf
                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A., AND PARTIAL SMEDLINE-93305254; PubMed-7765305,
                                                                                                                                                                                                                                                                                                                                                                                                                 Pseudomonas sp. (strain Al4).
Bacteria; Proteobacteria.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN-UW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DNA damage;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATP-binding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            64
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SUBCELLULAR LOCATION: Cytoplasmic (Potential).

SIMILARTY: BELONGS TO THE RECF FAMILY.

CAUTION: This entry seems to be produced by an incorrect sequence that contains at least 14 frameshifts. Do not use it for any
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FUNCTION: THE RECF PROTEIN IS INVOLVED IN DNA METABOLISM; IT IS REQUIRED FOR DNA REPLICATION AND NORMAL SOS INDUCIBILITY. RECF BINDS PREFERENTIALLY TO SINGLE-STRANDED, LINEAR DNA. IT ALSO SEEMS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        phylogenetic purpose.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LSSFKSQEL 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LSSFRSQRL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 364 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNA replication;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
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244
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                                                                                                                                                                                                                                              gamma-glutamyltranspeptidase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 33;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      POLY-ARG.
; BFF65FDB63AC8407 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNA-binding; SOS response; DNA repair;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ARG-RICH (BASIC).
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                                                                                                                                                                                                                                                                                                                                    SEQUENCE
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27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                 gene
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ID 64_MY
OS GN HH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Hypothetical protein MPN364 (H91_orf677).
MPN364 OR MPA72.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           YD64_MYCPN
P75417;
16-OCT-2001
16-OCT-2001
16-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LMYCPN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation—the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TIGRFAMS; TIGRO0066; g_glut_trans; 1.
PROSITE; PS00462; G_GLU_TRANSPEPTIDASE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR000101; Gglutrnspptdase.
Pfam; PF01019; G_glu_transpept; 1.
                                              InterPro; IPR004890; Lipoprotein_10.
InterPro; IPR004984; Lipoprotein_X.
Pfam; PF03202; Lipoprotein_10; 1.
Pfam; PF03305; Lipoprotein_X; 1.
                                                                                                                                                                                                  modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Complete sequence analysis of the genome of the bacterium Mycoplasma pneumoniae.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CHAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Transferase; Acyltransferase; Periplasmic; Zymogen; Signal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEROPS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; S63255; AAC60442.1;
                                                                                                                                                                                                                                                                                                                                                                                                                              Nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Himmelreich R., Hilbert H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=ATCC 29342 / m129;
MEDLINE-97105885; PubMed-8948633;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=2104;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacteria; Firmicutes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mycoplasma pneumoniae
                              Hypothetical
                                                                                                                                                       EMBL; AE000047; AAB96120.1;
                                                                                                                                                                                                                                                                                                 the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Herrmann R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        251
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                                                                                                                                                                                                                                                                                            SWISS-PROT entry is copyright. It is produced through a collable the Swiss Institute of Bioinformatics and the EMBL outst European Bioinformatics Institute. There are no restrictions
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377
450
575 AA;
       ol protein;
677 AA; 7
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376
575
6
450
61301 MW;
                                                                                                                                                                                                                                                                                                                                                                                                24:4420-4449(1996).
LONGS TO THE MG185 / MG260 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         54.58;
                            Complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mollicutes; Mycoplasmataceae; Mycoplasma.
     MW.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Plagens H., Pirkl E., Li B.-C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 33;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GAMMA-GLUTAMYLTRANSFERASE LARGE GAMMA-GLUTAMYLTRANSFERASE SMALL GAMMA-GLUTAMYL (POTENTIAL).
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     proteome.
E785B68BD679F04D CRC64;
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45;
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TP2A_CRIGR
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ovary cell line.";
J. Biol. Chem. 268.2160-2165(1993).
-:- FUNCTION: CONTROL OF TOPOLOGICAL STATES O
BREAKAGE AND SUBSEQUENT REJOINING OF DNA
MAKES DOUBLE-STRAND BREAKS.
-!- CATALYTIC ACTIVITY: ATP-dependent breakag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
DNA topoisomerase II, alpha isozyme (EC 5.9
TOP2A OR TOP2 OR TOP-2.
                                          NP_BIND
ACT_SITE
                                                                                                                                                                                                                                                                                                                        the European Bioinformatics Institute. There are no rest
use by non-profit institutions as long as its content
modified and this statement is not removed. Usage by an
entitles requires a license agreement (See http://www.isb-
or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cricetulus griseus (Chinese hamster).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
                                                                                             PRINTS: PRO0615; CCAATSUBUNTA.
PRINTS: PRO0418; TP12FAMILY.
ProDom: PD000745; DNA_topoisoIV;
ProDom: PD000742; DNA_topoisoIV;
SMART; SM00433; TOP2c; 1.
SMART; SM00434; TOP4c; 1.
                                                                                                                                                                               InterPro; IPR003957; CBFA_NFYB_top1s.
InterPro; IPR001241; DNA_topoisoII.
InterPro; IPR002205; DNA_topoisoIV.
Pfam; PF00204; DNA_gyraseB; 1.
Pfam; PF00521; DNA_topoisoIV; 1.
Pfam; PF02518; HATPase_C; 1.
                                                                                                                                                                                                                                                                               EMBL; L04607; AAA37023.1; ... HSSP; P06786; 1BGW.
                                                                                                                                                                                                                                                                                                                                                                                                                This
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01-NOV-1995
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                 between
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         topoisomerase II cDNA from an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Chan V.T., Ng S.W., Eder J.P., Schnipp
Molecular cloning and identification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. MEDLINE-93131977;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cricetulus
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                                                                                                                                                                                                                                                                   InterPro; IPR003594; ATPbind_ATPase
                             VARIANT
                                                                                   PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          243
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                                                                                                                                                                                                                                                                                                                                                                                                                                      SUBUNIT: HOMODIMER.
SUBCELLULAR LOCATION: Nuclear.
MISCELLANEOUS: EUKARYOTIC TOPOISOMERASE I AND II CAN RELL
NEGATIVE AND POSITIVE SUPERCOILS, WHEREAS PROKARYOTIC ENT
RELAX ONLY NEGATIVE SUPERCOILS.
SIMILARITY: BELONGS TO THE TYPE II TOPOISOMERASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         of double-stranded DNA.
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                           Topoisomerase; 1
160 165
804 804
493 493
 1526
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₽,
             TOPOISOMERASE_II; 1.

comerase; DNA-binding; ATP-binding; Nuclear protein.

165 ATP (POTENTIAL).

804 DNA CLEAVAGE (BY SIMILARITY).

493 R -> Q (IN CELLS RESISTANT TO THE

ANTINEOPLASTIC AGENTS VP-16 AND VM-26).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PubMed-8380592;
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 173196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              annotation update)
isozyme (EC 5.99.1.3).
 Æ;
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         , Schnipper L.E.;
fication of a point mutation
etoposide-resistant Chinese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Schnipper L. ication of a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OF DNA BY STRANDS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         passage and
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                                                                                                                                                                                                                                                                                                                                                        and
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SOUTH AND DESCRIPTION OF THE PROPERTY OF THE P
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Best Local Similarity
7; Conserv
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                                                                                                                       Pfam; PF00204; DNA_gyrase; 1.
Pfam; PF00521; DNA_topoisoIV; 1.
Pfam; PF005218; HATPASe_C; 1.
PRINTS; PR00615; CCAATSUBUNTA.
PRINTS; PR00418; TP12FAMILY.
Pr0Dom; PD000742; DNA_topoisoII; 1
Pr0Dom; PD000742; DNA_topoisoIV; 1
SMART; SM00433; TOPAC; 1.
SMART; SM00434; TOPAC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for comentitles requires a license agreement (See http://www.isb-sib.ch/an or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Biochem. Biophys. Res. Commun. 193:787-793(1993).

1. FUNCTION: CONTROL OF TOPOLOGICAL STATES OF DNA BY
BREAKAGE AND SUBSEQUENT REJOINING OF DNA STRANDS.

MAKES DOUBLE-STRAND BREAKS.

1. CATALYTIC ACTIVITY: ATP-dependent breakage, passag
of double-stranded DNA.

1. SUBUNIT: HONODIMER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence up
16-OCT-2001 (Rel. 40, Last annotation
DNA topoisomerase II, alpha isozyme (E
TOP2A OR TOP2 OR TOP-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TP2A_RAT P41516;
                                                                                                                                                                                                                                                                                                                                                     InterPro;
InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRALN-Sprague-Dawley; TISSUE-Testis; MEDLINE-93290677; PubMed-8390253; Park S.H., Yoon J.H., Kwon Y.D., Park S.D. "Nucleotide sequence analysis of the CDNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa;
Mammalia; Eutheria;
NCBI_TaxID=10116;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rattus norvegicus (Rat).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RELAX ONLY NEGATIVE SUPERCOILS.
SIMILARITY: BELONGS TO THE TYPE II TOPOISOMERASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SUBCELLULAR LOCATION: Nuclear.
MISCELLANEOUS: EUKARYOTIC TOPOISOMERASE I
NEGATIVE AND POSITIVE SUPERCOILS, WHEREAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DLSSFKSQEL
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Z19552;
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P06786;
PS00177; TOPOISOMERASE_II; 1.

je; Topoisomerase; DNA-binding; ATP-binding; Nuclea 159 164 ATP (POTENTIAL).

8 803 DNA CLEAVAGE (BY SIMILARITY).

8 1526 AA; 173220 MW; A1961ABBDB1B050F CRC64;
                                                                                                                                                                                                                                                                                                                                                  IPR003594; ATPbind_ATPase.
IPR003957; CBFA_NFYB_topis.
IPR001241; DNA_topoisoII.
IPR002205; DNA_topoisoIV.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      1BGW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -; NOT_ANNOTATED_CDS
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Rodentia;
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; Murinae; Rattus.
                                                                              Nuclear
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01-APR-1993
01-APR-1993
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                      Pfam;
Pfam;
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EMBL; U01915; AAC55135.1; -.
PIR; JS0703; JS0703.
PIR; S35483; S35483.
HSSP; P06786; 1BGW.
                                                                                                                                                                                                                                                                                                                                   between the Swiss Institute of Bioinformatics the European Bioinformatics Institute. There a use by non-profit institutions as long as a modified and this statement is not removed. Use entitles requires a license agreement (See http or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     messenger RNA transcript encoding topoisomerase retinoic acid receptor alpha locus.";
Cancer Res. 53:5885-5889(1993)
-i- FUNCTION: CONTROL OF TOPOLOGICAL STATES OF UNREAKAGE AND SUBSEQUENT REJOINING OF DNA STR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE-Lymphoma;

MEDLINE-94084643; PubMed-8261398;

MCPherson J., Brown G.A., Goldenberg G.J.;

"Characterization of a DNA topoisomerase IIalpha gene rearrangement in adriamycin-resistant P388 leukemia; expression of a fusion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.

MEDLINE-93065194; PubMed-1331984;
Adachi N., Miyaike M., Ikeda H., Kikuchi A.;

"Characterization of cDNA encoding the mouse that can complement the budding yeast top2 mu Nucleic Acids Res. 20:5297-5303(1992).
                                                                                                                                                                      MGD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -i- MISCELLANEOUS: EUKARYOTIC TOPOISOMERASE I AND II CAN REL
NEGATIVE AND POSITIVE SUPERCOILS, WHEREAS PROKARYOTIC EN
RELAX ONLY NEGATIVE SUPERCOILS.
-i- SIMILARITY: BELONGS TO THE TYPE II TOPOISOMERASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MAKES DOUBLE-STRAND BREAKS.
-I- CATALYTIC ACTIVITY: ATP-dependent breakage,
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Mammalia; Eutheria;
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                                                                                                                                           InterPro;
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                                                               MGI:98790; Top2a.
irPro; IPR003594; ATPbind_ATPase.
irPro; IPR003957; CGBFA_NEYB_top1s.
irPro; IPR001241; DNA_top01s0II.
irPro; IPR002205; DNA_top01s0IV.
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7; Conser
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(Rel. 40, Last annotation)
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Rodentia;
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Pred. No. 1.3e+02;
0; Mismatches 3;
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DR PRINTS; PRO0615; CCAATSUBUNTA.
DR PRINTS; PRO0418; TPIZFAMILY.
DR PRINTS; PRO0418; TPIZFAMILY.
DR PRODOM; PD0000742; DNA_topoisoIV; 1.
DR SMART; SM00433; TOP2C; 1.
DR SMART; SM00433; TOP2C; 1.
DR SMART; SM00433; TOP2C; 1.
DR PROSITE; PS00177; TOPOISOMERASE_II; 1.
KW ISOMERASE; Topoisomerase; DNA-binding; Nuclear protein.
ET NP_BIND 160 165 ATP (POTENVIAL).
STITE 804 804 DNA CLEAVAGE (BY SIMILARITY).
SQ SEQUENCE 1528 AA; 172876 MW; 9061778DCA6C756A CRC64;
Ouery Match 64.7%; Score 33; DB 1; Length 1528;
Best Local Similarity 70.0%; Pred. No. 1.3e+02;
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 2 DLSSFKSQEL 11
Db 221 DLSKFKMQSI 230

Search completed: March 13, 2003, 18:49:53
Job time: 8.8 secs
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ALIGNMENTS

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F;1-7, D, 43-321/Product: IGE FG receptor II. splice form a' #status predicted < F;14-20/Region: stop-transfer sequence F;24-45/Domain: transmembrane #status predicted <TMM> F;46-321/Domain: transmembrane #status predicted <EXT> F;46-84/Region: 21-residue repeat F;81-321/Droduct: soluble IgE-binding factor (37K) #status predicted <IGE> F;81-321/Product: soluble IgE-binding factor (33K) #status predicted <IGE> F;102-321/Product: soluble IgE-binding factor (29K) #status predicted <IGE> F;106-126/Region: 21-residue repeat F;102-321/Product: soluble IgE-binding factor (25-27K), long form #status experi F;149-321/Product: soluble IgE-binding factor (25-27K), short form #status experi F;163-282/Domain: C-type lectin homology <LCH> F;63/Binding site: carbohydrate (Asn) (Covalent) #status predicted F;147-148/Cleavage site: Mys-Leu (unidentified proteinase) #status experimental F;149-150/Cleavage site: Arg-Met (unidentified proteinase) #status experimental F;191-282,259-273/Disulfide bonds: #status experimental
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A;Map position: 19p13.3-19p13.3
A;Map position: 19p13.3-19p13.3
A;Introns: 8/1; 46/1; 64/1; 85/1; 106/1; 127/1; 157/1; 207/3; 243/2
C;Superfamily: 1gE receptor II; C-type lectin homology
C;Keywords: alternative splicing; B-cell; glycoprotein; immunoglobulin receptor; macroph F; MNPPSQD', 47-321/Product: 1gE Fc receptor II, splice form b' #status predicted <SFBI>F; MNPPSQD', 8-321/Product: 1gE Fc receptor II, splice form a #status predicted <SFB>F;1-321/Product: 1gE Fc receptor II, splice form a #status predicted <SFA>F;1-321/Product: 1gE Fc receptor II, splice form a #status predicted <SFA>F;1-7,'U', 47-321/Product: 1gE Fc receptor II, splice form a' #status predicted <SFAI>F;1-7,'U', 47-321/Product: 1gE Fc receptor II, splice form a' #status predicted <SFAI>F;1-7,'U', 47-321/Product: 1gE Fc receptor II, splice form a' #status predicted <SFAI>F;1-7,'U', 47-321/Product: 1gE Fc receptor II, splice form a' #status predicted <SFAI>F;1-7,'U', 47-321/Product: 1gE Fc receptor II, splice form a' #status predicted <SFAI>F;1-7,'U', 47-321/Product: 1gE Fc receptor II, splice form a' #status predicted <SFAI>F;1-7,'U', 47-321/Product: 1gE Fc receptor II, splice form a' #status predicted <SFAI>F;1-7,'U', 47-321/Product: 1gE Fc receptor II, splice form a' #status predicted <SFAI>F;1-7,'U', 47-321/Product: 1gE Fc receptor II, splice form a' #status predicted <SFAI>F;1-7,'U', 47-321/Product: 1gE Fc receptor II, splice form a' #status predicted <SFAI>F;1-7,'U', 47-321/Product: 1gE Fc receptor II, splice form a' #status predicted <SFAI>F;1-7,'U', 47-321/Product: 1gE Fc receptor II, splice form a' #status predicted <SFAI>F;1-7,'U', 47-321/Product: 1gE Fc receptor II, splice form a' #status predicted <SFAI>File Richard Receptor II, splice form a' #status predicted <SFAI>File Richard Receptor II, splice form a' #status predicted <SFAI
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A;Reference number: A65963; PDB:1KJE
A;Reference number: A65963; PDB:1KJE
A;Contents: annotation; conformation by theoretical model, residues 173-285
C;Comment: The sequence of the splice form a is shown.
C;Comment: This receptor for the Fc portion of IgE is expressed in various hematopoletic ells.
C;Comment: Splice form a is expressed constitutively in B-cells; b is expressed in other C;Comment: Soluble IgE-binding factors are produced by proteolytic cleavage of IgE Fc re C;Genetics:
A;Gene: GDB:FCER2; FCE2
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A; Residues: 'MNPPSO', B-14 <YOK>
A; Residues: 'MNPPSO', B-14 <YOK>
A; Residues: 'MNPPSO', B-14 <YOK>
A; Cross-references: GB:M23562; NID:g182444
A; Experimental source: splice form IIb
A; Experimental source: perfect, M.; Delespesse, G.
Mol. Immunol. 26, 1105-1112; MSP
A; Title: Mechanisms of formation of IgE-binding factors (soluble CD23)-I. Fc epsilon:
A; Reference number: JL0132; MUID:90220658; PMID:2534424
A; Accession: JL0132
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A;Residues: 152-166;173-179;189-212;230-263;268-306 <ROS>
R;Padlan, E.A.; Helm, B.A.
submitted to the Brookhaven Protein Data Bank, June 1993
A;Reference number: A51791; PDB:1HLI
A;Contents: annotation; conformation by theoretical model, residues 173-285
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A:Title: Partial characterization of natural and recombinant human soluble CD23 A;Reference number: S29107; MUID:93038513; PMID:1417742
A;Accession: S29107
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A;Note: part of this sequence, including the amino end of soluble forms of the protein, R;Yokota, A.; Kikutani, H.; Tanaka, T.; Sato, R.; Barsumian, E.L.; Suemura, M.; Kishimot Cell 55, 611-618, 1988
A;Title: Two species of human Fc-epsilon receptor II (Fc-epsilon-RII/CD23): tissue-specia;Reference number: A31924; MUID:89028672; PMID:2972386
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A; Accession: A26589
A; Molecule type: mRNA
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                       Matches
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Query Match

100.0%;

Score 51;

DB 1;

Length 321;

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ADLSSFKSQEL 11

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A; Molecule type: DNA
A; Molecule type: DNA
A; Residues: 1-4131 <WIL>
A; Cross-references: EMBL: Z75536; PIDN: CAA99830.1; GSPDB: GN00019; CESP: F18C12.1
A: Evnerimental source: clone F18C12
                                                                   A:Map position: 1
A:Introns: 54/3; 112/3; 146/1; 294/1; 381/3; 455/3; 596/3; 716/3; 743/2; 782/3; 820/3
09/3; 2303/3; 2403/1; 2529/1; 2612/3; 2687/1; 2734/3; 2799/3; 2841/3; 2891/2; 2932/3;
C;Superfamily: dynein heavy chain, cytosolic
                                                                                                                                                                                                                                                                                                                                                                hypothetical protein F18C12.1 - Caenorhabditis elegans
(;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 17-Mar-2000
C;Accession: T21085
R;Harris, B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   submitted to the EMBL Data Library, A; Reference number: Z19501 A; Accession: T22009
                                                                                                                                                                                                                                                                                                                        submitted to the EMBL Data Library, June A; Reference number: Z19371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: EMBL:Z81098; PIDN:CAB03184.1; A;Experimental source: clone K07A12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     submitted to the EMBL Data Library, October 1996
A;Reference number: Z19735
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A;Experimental source: clone F39H2
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A; Residues: 1-305 <W
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C;Accession: T22009; T23398
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Best Local
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Similarity
8; Conserv
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8; Conserv
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1; Mismatches
                  Pred.
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R;Carrington, M.; Miller, N.; Blum, M.; Roditi, I.; Wiley, D.; Turner, M. J. Mol. Biol. 221, 823-835, 1991
A;Title: Variant specific glycoprotein of Trypanosoma brucei consists of two A;Reference number: $18445; MUID:92046037; PMID:1942032
A;Accession: $18449
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S18449
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C;Specias: Leishmania tropica
C;Specias: Leishmania tropica
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 31-Jan-2000
C;Accession: T18344
R;Lafuente, E.; Castanys, S.; Gamarro, F.
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C;Accession: C8293
                                                                                                                                                                                                                                                                                                   variant surface glycoprotein ILTat 1.24 - Trypanosoma brucei C;SpecLes: Trypanosoma brucei C;DecLes: Trypanosoma brucei C;Date: 16-Sep-1992 *sequence_revision 16-Sep-1992 *text_change 20-Aug-1999 C;Accession: S18449
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A;Cross-references: EMBL:U55381; NID:g1916605; PID:g1916606; PIDN:AAB51191.1
C;Superfamily: human multidrug resistance protein cMOAT2; ATP-binding cassette homology
A; Cross-references: EMBL: X56767; NID: g10453; C; Superfamily: variant surface glycoprotein
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A; Accession: C82938
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                                                                    A; Molecule type: mRNA
A; Residues: 1-514 <CAI
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A; Accession: T18344
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A;Genetic code: SGC3
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A; Residues: 1-293 <GLA>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     preliminary; translated from GB/EMBL/DDBJ
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                                                                 .-514 <CAR>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DNA
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Pred. No.
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15;
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                                  PIDN:CAA40086.1; PID:g10454
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probable methyltransferase
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C.Accession: S50479
R;Dietrich, F.S.
submitted to the EMBL Data Library, December submitted to the sequence of S. cerevisiae
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S50479
                                                                                                                                                                                                                                                                                                                               GCN1 homolog - fission yeast (Schizosaccharomyces pombe)
C;Species: Schizosaccharomyces pombe
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 07-Dec-1999
                                                                                                                                                                                                                                                                                                                                                                                  RESULT
T37919
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Map position:
C; Superfamily:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Gene: SGD:RPN3; SUN2; MIPS:YER021w
A;Cross-references: SGD:S0000823; MIPS:YER021w
A;Map position: 5R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Species: Saccharomyces cerevisiae
C;Date: 28-May-1993 #sequence_revision
C;Accession: S50479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            26S proteasome regulatory particle chain RPN3 - N;Alternate names: protein YER021w
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
7; Conserve
                                                                                                                                                                                                                                                                                      R;Connor, R.; Churcher, C.M.; Barrell, B.G.; Rajandream, M.A.; submitted to the EMBL Data Library, December 1995
                                                                                                                                                                                                                                                                                                                                                               GCN1 homolog -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: DNA
A; Residues: 1-523 <DIE>
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                                                                                                                      A; Introns: 50/1
                                                                                                                                                                   C; Genetics:
                                                                                                                                                                                 A; Experimental source:
                                                                                                                                                                                                             A; Molecule type: DNA
A; Residues: 1-2670 <CON>
                                                                                                                                                                                                                                                        A; Reference number: 221754
A; Accession: T37919
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: EMBL:U18778; NID:g603592; PID:g603613; GSPDB:GN00005; MIPS:YER02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Reference number: S50433
                                                                                                                                    A; Map position:
                                                                                                                                                    A; Gene:
                                                                                                                                                                                                 A; Cross-references:
                                                                                                                                                                                                                                           A;Status:
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Best Local S
Matches 7
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Best Local 9
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                              1 ADLSSFKSQEL 11
                                                                                                                                                   SPDB:SPAC18G6.05c
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ADTSNFSNQEL
                                                        Similarity 7; Conserv
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7; Conserv
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682
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                                                                                                                                                                               PIDN:CAA92385.1;
2h-; cosmid c18G6
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                                                                        Score 35;
Pred. No.
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Pred. No.
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43;
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2.3e+02;
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Chlamydia

trachomatis (serotype D, strain UW3/Cx)

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R;Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berter C.; Bron, S.; Broullet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Cha A.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E. Nature 390, 249-256, 1997

Nature 390, 249-256, 1997

N; Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galler iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F. Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois, A; Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueelly, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadale, Y.; Sato, T.; Scanlon, A; Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiquchi, J.; Sekowska, A.; Serottekeni, M.; Tamako, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchlyama, T.; Winters, P.; Wipat, A.; Tamamoto, H.; Kamane, K.; Yasunoto, K.; Yata, K.; Yoshida, K.; Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.; A:Gersaio, D. Rose, MUID:98044033; PMID:9384377
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A;Molecule type: DNA
A;Residues: 1-170 <ARN>
A;Residues: 1-170 <ARN>
A;Cross-references: GB:AE001321; GB:AE001273; NID:g3328906; PIDN:AAC68077.1; PID:g332891
A;Cross-references: GB:AE001321; GB:AE001273; NID:g3328906; PIDN:AAC68077.1; PID:g332891
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                                                                                                                                                                                                                                                                                                                                                                                                            C;Superfamily: short-chain ATP-binding cassette proteins;
C;Keywords: ATP; nucleotide binding; P-loop
F;21-216/Domain: ATP-binding cassette homology <ABC>
F;38-45/Region: nucleotide-binding motif A (P-loop)
         hypothetical protein F31E8.6 - Caenorhabditis elegans C;Species: Caenorhabditis elegans
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: GB:Z99111; GB:AL009126; NID:g2633699; PIDN:CAB13309.1; A;Experimental source: strain 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Residues: 1-230 <KUN>
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A:Accession: B71510
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C:Date: 13-Sep-1998 #sequence_revision 13-Sep-1998 #text_change 08-Oct-1999
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                                                                                                                                                                                                                                                                                                      Matches
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7; Conserv
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                                                                                                                                                                                                                                                                                                Score 34; DB
Pred. No. 30;
3; Mismatches
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Pred. No.
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C;Keywords: glycoprotein; serine proteinase inhibitor F;1-23/Domain: signal sequence #status predicted <SIG>F;1-23/Domain: signal sequence #status predicted <SIG>F;24-40/Domain: plasminogen activator inhibitor 1 #status predicted <MAT>F;232,288,352/Binding site: carbohydrate (Asn) (covalent) #status predicted F:369/Inhibitory site: Arg (plasminogen activator) #status predicted
                                                                                                                                                                                                                                                                                                        A; Molecule type: protein
A; Residues: 24-49; L',51-63 <KAT>
C; Comment: Three types of PAI have been identified. PAI-1
may be the primary site of synthesis of plasma PAI.
C; Comment: This inhibitor acts as "bait" for tissue plasmi
                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: mRNA
A; Residues: 153-235 CPEP>
A; Cross references: EMBL:X52906; NID:g598; PIDN:CAA37094.1; PID:g930005
A; Cross references: EMBL:X52906; NID:g598; PIDN:CAA37094.1; PID:g930005
R; Katagiri, K.; Okada, K.; Hattori, H.; Yano, M.
Eur. J. Biochem. 176, 81-87, 1988
A; Title: Bovine endothelial cell plasminogen activator inhibitor. Purification and A; Reference number: S01324; MUID:88329072; PMID:3262060
A; Accession: S01324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A:Cross-references: EMBL:X16383; NID:g600; PIDN:CAA34419.1; R;Pepper, M.S.; Belln, D.; Montesano, R.; Orci, L.; Vassalli J. Cell Biol. 111, 743-755, 1990
A;Title: Transforming growth factor-beta 1 modulates basic fa;Reference number: A35855; MUID:90338128; PMID:1696269
A;Accession: A35855
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S06745
                                                                                                                                                                                                                                 C; Comment: Glycosylation is not a prerequisite for C; Superfamily: antithrombin III
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          plasminogen activator inhibitor-1 precursor - bovine N;Alternate names: endothelial-cell plasminogen activator inhibitor; PAI-1 C;Species: Bos primigenius taurus (cattle) C;Date: 28-Feb-1990 #sequence_revision 22-Apr-1995 #text_change 18-Jun-1999 C;Accession: S06745; A35855; S01324; S19906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R:Mimuro, J.; Sawdey, M.; Hattori, M.; Luskutoff, D.J.
Nucleic Acids Res. 17, 8872, 1989
A;Tille: CDNA for bovine type 1 plasminogen activator inhibitor (PAI-1).
A;Reference number: S06745; MUID:90067867; PMID:2587231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: mRNA
A; Residues: 1-402 <MIM>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: DNA
A; Residues: 1-270 < DUZ>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Accession:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Map position:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Gene:
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Pred. No.
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Mismatches
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A;Residues: 1-1046 <STO>
A;Cross-references: GB:AE005176; PID:g12724301; PIDN:AAK05419.1; GSPDB:GN00146
A;Experimental source: strain IL1403
C;Genetics:
A;Gene: sbcC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            submitted to the Protein Sequence Database, April 1996
A; Reference number: S62944
A; Reference number: S6394
A; Accession: S6397
A; Molecule type: DNA
A; Residues: I-1116 <DUE>
A; Cross-references: EMBL: Z71680; NID:g1302593; PID:e239847; PID:g1302594; GSPDB:GN00014;
A; Experimental source: Strain S288C
C; Genetics:
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A;Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis sea, Reference number: A86625; MUID:21235186; PMID:11337471
A;Accession: A86790
A;Status: preliminary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Gene: MIPS:YNR065c
A;Cross-references: SGD:S0005348
A;Map position: 148
C;Keywords: transmembrane protein
F;941-957/Domain: transmembrane #status p
F;990-1006/Domain: transmembrane #status
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               probable membrane protein YNR065c - yeast (Saccharomyces cerevisiae)
N;Alternate names: hypothetical protein N3539
C;Species: Saccharomyces cerevisiae
C;Date: 27-Apr-1996 #sequence_revision 03-May-1996 #text_change 19-Apr-2002
C;Accession: S63397
R;Duesterhoeft, A.; Floeth, M.; Fritz, C.; Heuss-Neitzel, D.; Hilbert, H.; Moestl, D.
                                                                               hypothetical protein HP0256 - Helicobacter pylori (strain 26695)
C;Species: Helicobacter pylori
C;Date: 09-Aug-1997 *sequence_revision 09-Aug-1997 *text_change 08-Oct-1999
C;Accession: H64551
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R;Tomb, J.F.; White, O.; Kerlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.D. Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khalak, H.G.; Glodek, A.; McKenneson, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Watthey, L.
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Pred. No. 1.5e+0
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Pred. No. 1.4e+02;
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Nature 388, 539-547, 1997
A;Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fras. A;Title: The complete genome sequence of the gastric pathogen Helicobacter pylori. A;Reference number: A64520; MUID:97394467; PMID:9252185
A;Accession: H64551
Search completed: March 13, 2003, 18:52:57 Job time : 12.8 secs
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                                                                                                                                                                                                                                                   A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Molecule type: DNA A;Residues: 1-142 <TOM>
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                                                                                                                                                          Matches
                                                                                                                                                                                             Query Match
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                                                                                                                  1 ADLSSFKSQEL 11
                                                                               AQLSAFKNPEL 52
                                                                                                                                                          Similarity 7; Conserv
                                                                                                                                                          Conservative
                                                                                                                                                                        64.7%;
                                                                                                                                                      Score 33; DB:
Pred. No. 29;
2; Mismatches
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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Perfect score:
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                                                                                                                                                                                                                                                                                                    Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                           Score
   US-10-050-200-4
                                                                                                                                                                                                         Query
Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        March 13, 2003, 18:40:08; Search time 29.2 Seconds
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/SIDSI/gcgdata/geneseq/geneseqp-embl/AA1990.DAT:
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                                                                                                                                                                                                           Length
166
167
320
321
321
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                     18
18
9
9
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9
               AAW13146
AAW13148
AAW13143
AAP70105
AAP82073
AAP81163
AAP81130
AAP81172
AAP81172
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                                                                                                                                                                                                                                                                  SUMMARIES
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50.197 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       908470
             Human soluble CD23
Human soluble CD23
Sequence containin
IgE binding factor
Recombinant Fc_eps
Low affinity Fc_ep
Fc gamma receptor.
Human IgE binding
Sequence encoded b
                                                                                                                                                                                                     Description
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32	32	32	32	32	32	32	32	32	32	32	33	33	33	33	ω ω	33	ω S	33	33	34	34	35	35	35	35	36	36	36	38	38	51	51	51	51
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314	312	306	274	274	270	270	210	81	45	42	659	507	378	377	309	205	174	91	91	1046	170	1310	361	327	183	306	289	289	50	50	336	321	321	321
21	22	21	21	21	21	21	21	21	21	21	21	22	23	23	22	23	17	22	22	23	20	22	21	20	22	22	21	21	22			18	14	10
AAY54114	AAG62614	AAG06929	AAG44263	AAG12783	AAG45071	AAG23242	AAG33820	AAG59806	AAG59807	AAG59808	AAB25107	AAB92617	AAE21814	AAE21827	AAU04910	ABB47747	AAR88503	AAU14597	AAU14361	ABB54658	AAY37747	ABB63443	AAB53264	AAY41679	ABB68544	ABB06927	AAY43796	AAY54094	Φ	ABB96396	AAP82839	AAW13142	AAR42053	AAP90367
A GDP-4-keto-6-deo	A thaliana GDP-4-k	Arabidopsis thalia	Arabidopsis thalia	Arabidopsis thalia	thal	thal			Arabidopsis thalia	Arabidopsis thalla	Eucalyptus grandis	-		Human 46873 aspara	Micromonospora eve	Listeria monocytog	Borrelia burgdorfe		Human novel protei	Lactococcus lactis	Chlamydia trachoma	Drosophila melanog	Human colon cancer	Human H-beta 58 fa	Drosophila melanog	nonosp	acid s	Enzyme EPSI involv		Human testicular a		uence contai	D.	Peptide sequence o

ALIGNMENTS

RESULT 1 AAW13146

AAW13146 standard; Protein; 166 AA

Human soluble CD23 isoform D.

17-JUN-1997 AAW13146;

(first entry)

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(LYNC/) LYNCH R G. (MATS/) MATSUI M. (NUNE/) NUNEZ R M. (YODO/) YODOI J.
DNA sequence encoding a soluble isoform of CD23 - scale preparation of the protein
                     WPI; 1997-159094/15.
N-PSDB; AAT61959.
                                                                                  28-DEC-1994;
                                                                                                  27-DEC-1995;
                                                                                                                 04-FEB-1997.
                                                                                                                               JP09028385-A.
                                                                                                                                               Homo sapiens
                                                                                                                                                            Human; soluble; CD23; complementarity determining; isoform D; recombinant production.
                                                                                  94US-0365103
                                                                                                  95JP-0341169
        useful for large
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AAP90120

Human lymphocyte

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RESULT 2
AAW131.48
ID AAW1
AXX
AAW11
AXX
AAW1
AXX
AAW1
AXX
AW1
AXX
AW1
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Best Local S
Matches 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (LYNC/) LYNCH R G. (MATS/) MATSUI M. (NUNE/) NUNEZ R M. (YODO/) YODOI J.
                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                     The cDNA encoding the present sequence, human soluble CD23 isoform C, can be used for the large scale recombinant proof soluble CD23.
                                                                                                                                                                                     The specification states that the nucleotide sequences contained in figures 4a-b, 5a-b, 12a-12b and 13a-b are claimed, however thinumbering scheme does not relate to the scheme used in the releving sections of the specification.
                                                                                                                                                                                                                                                                                                                                                                               Claim 1; Figure 15; 33pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                              DNA sequence encoding a soluble isoform scale preparation of the protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The specification states that the nucleotide sequences contained in figures 4a-b, 5a-b, 12a-12b and 13a-b are claimed, however this numbering scheme does not relate to the scheme used in the relevant sections of the specification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1997-159094/15.
N-PSDB; AAT61961.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             04-FEB-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           JP09028385-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; soluble; CD23; complementarity determining; isoform C; recombinant production.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17-JUN-1997 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAW13148 standard; Protein; 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    of soluble CD23.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The cDNA encoding the present sequence, human soluble CD23 isoform D, can be used for the large scale recombinant pro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28-DEC-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            27-DEC-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human soluble CD23
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                                            Local Similarity
nes 11; Conserv
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  H
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  ADLSSFKSQEL 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               166 AA;
                                                                                                                                           167 AA;
                                       100.0%;
ilarity 100.0%;
Conservative 0
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Pred. No.
                                                               Score 51; DB 18
Pred. No. 0.058;
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                                              Mismatches
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                                                                                        Length 167;
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                                              Indels
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                                                                                                                                                                                                                                                                                                        production
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RESULT 4
AAP70105
ID AAP7
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AC AAP7
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AC AAP7
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Best Local S
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(MATS/) MATSUI M.
(NUNE/) NUNEZ R M.
(YODO/) YODOI J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Key
Peptide
                                                                                                                                                                                                       The cDNA encoding the present sequence, which contains human soluble CD23 isoform B, can be used for the large scale recombinant production of soluble CD23.

The specification states that the nucleotide sequences contained in figures 4a-b, 5a-b, 12a-12b and 13a-b are claimed, however this numbering scheme does not relate to the scheme used in the relevant sections of the specification.
                            04-FEB-1991
                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                      DNA sequence encoding a soluble isoform scale preparation of the protein
                                                                                                                                                                                                                                                                                                                                  WPI; 1997-159094/15
N-PSDB; AAT61956.
                                               AAP70105;
                                                                AAP70105 standard;
                                                                                                                                                                                                                                                                                   Claim 1; Pages 18-20; 33pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                             28-DEC-1994;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   JP09028385-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; soluble; CD23; complementarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence containing human soluble CD23 isoform B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17-JUN-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAW13143;
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        IgE binding factor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            isoform
                                                                                                                117
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                                                                                                                       1 ADLSSFKSQEL 11
                                                                                                              ADLSSFKSQEL 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADLSSFKSQEL
                                                                                                                                                    11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           B; recombinant production
                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              standard; Protein;
                                                                                                                                                                                         320 AA;
                                                                                                                                                    Conservative
                           (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first
                                                                                                                                                                                                                                                                                                                                                                                                             94US-0365103
                                                                                                                                                                                                                                                                                                                                                                                                                               95JP-0341169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             90
                                                                protein;
                                                                                                                                                            100.0%;
                           entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "soluble CD23 isoform
                                                                 321
                                                                                                                                                    0;
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                                                                                                                                                            Score 51;
Pred. No.
                                                                 A.
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                                                                                                                                                                      B
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                                                                                                                                                                     18;
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Query Match
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04-SEP-1986;
05-SEP-1986;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 The protein reacts with anti-Fc epsilon receptor antibody, and is obtd. In large quantities. The DNA encoding the protein is obtd. from, eg human B cells, human malignant B or T cells, human monocytes or human ensinophilic cells. RPMI 8866 cells may also be cultured to produce the mRNA. The IgE binding factor and Fc epsilon receptor binds IgE and can be used to enhance the prodn. of IgE from IgE producing cells. They can be used to treat allergies by eliminating excess blood IgE, and can also
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 6; page 42-3; 57pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1987-343202/49.
N-PSDB; AAN70107.
                                                                                                                Domain
                                                                                                                                                                                         Low affinity
                                                                                                                                                                                                              Recombinant Fc_epsilon receptor.
                                                                                                                                                                                                                                     17-OCT-1990
                                                                                                                                                                                                                                                            AAP82073;
                                                                                                                                                                                                                                                                                AAP82073 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Honjo T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (KURS ) KURARAY CO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        29-APR-1987;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IgE
  Cleavage-site
                                                                    Domain
                                                                                                                                                                    Homo sapiens
                                    Modified-site
                                                                                                                                     Domain
                                                                                                                                                                                                                                                                                                                                        118 ADLSSFKSQEL 128
                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
                                                                                                                                                                                                                                                                                                                                                   1 ADLSSFKSQEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IgE binding factor protein - obtd. by culturing cells harbouring
ss specific Fc receptor on their surface.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               binding factor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Yodoi J,
                                                                                                                                                                                                                                                                                                                                                                                                                               321 AA;
                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                          Ç
                                                                                                                                                                                                                                    (first entry)
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86JP-0209091.
86JP-0210429.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        87EP-0106265
                                  /label-transmembrane region /note-"hydrophobic residues" 63..63
  /label*glycosylation_site
/note*"N-linked"
149..150
                                                                   /label-stop_transfer_seq
/note-"basic cluster involved
integration into bilayer"
22..47
                                                                                                                                     Location/Qualifiers 1..21
                                                                                                                                                                                         epsilon
                                                                                                                                                                                                                                                                                                                                                              11
                                                                                                                         /note="hydrophilic N-terminal"
                                                                                                                                                                                                                                                                                protein; 321 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Takami
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FC
                                                                                                                                                                                                                                                                                                                                                                                            100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             epsilon receptor; allergy; RPMI 8866 cells;
                                                                                                                                                                                         receptor; IgE; allergy.
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                                                                                                                                                                                                                                                                                                                                                                                            Score 51; DB 8;
Pred. No. 0.12;
                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                   0;
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                                                                                                                                                                                                                                                                                                                                                                                                       Length 321;
                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                  0,
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                                                                                                                                                                                                                                                                                                                                                                                   0
                                                                                                                                                                                                                                                                                                                RESULT 6
AAP81163
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Best Local Similarity
""+"hes 11; Conserve
  В
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   SXCCCCXXX PTTX RXX RXX RXX PXX PTTTT
                                                                                                                                                                                         Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNA encoding the sequence or a part of it can be used to make recombinant receptor which is useful for treating IgE allergic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New human low affinity Fc(epsilon)-receptor and parts for treating local or systemic allergic reactions and recombinant DNA methods.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1988-065437/10.
P-PSDB; AAP82073.
New human lower affinity Fc(epsilon)-receptor - useful for treating
                       WPI; 1988-057531/09
N-PSDB; AAN81485.
                                                       Kishimoto T,
                                                                             (KISH/) KISHIMOTO T.
                                                                                                   21-AUG-1986;
                                                                                                                        21-AUG-1986;
                                                                                                                                             02-MAR-1988
                                                                                                                                                                   EP257114-A.
                                                                                                                                                                                                             Low affinity
                                                                                                                                                                                                                                   Low affinity
                                                                                                                                                                                                                                                          15-OCT-1990
                                                                                                                                                                                                                                                                                AAP81163;
                                                                                                                                                                                                                                                                                                      AAP81163 standard; protein; 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         reactions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 4; Page 39; 59pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Kishimoto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (CELL-) CELLULAR IMMUNOLOGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21-AUG-1986;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23-SEP-1986;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EP258489-A.
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118 ADLSSFKSQEL 128
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                                                                                                                                                                                        sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                              Fc_epsilon receptor; IgE; allergy
                                                                                                                                                                                                                                   Fc_epsilon receptor encoded by gene carried by pGEM4.
                                                                                                                                                                                                                                                         (first entry)
                                                       Suemura
                                                                                                                                                                                                                                                                                                                                                                                                                                                   ξ,
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                                                                                                   86EP-0111581.
                                                                                                                         86EP-0111581
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /label=soluble
/note="Claim 7"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="target for trypsin-like proteases"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /label=membrane_bound
                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%;
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                                                       Kikutani
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                                                                                                                                                                                                                                                                                                                                                                                                         0
                                                                                                                                                                                                                                                                                                                                                                                                                  Score 51; DB 9
Pred. No. 0.12;
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                                                       Barsumian
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                                                       EL;
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RESULT 8
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AC AAP8
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Best Local S
Matches 11
                                                                                                                                                       Query Match
Best Local Similarity
Matches 11; Conserv
 Human IgE binding factor related polypeptide
                      12-DEC-1990
                                                                                                                                                                                                                   Fe epsilon receptor binds IgE. It is expressed from cell line RPMI8866. It is expressed in large ants, and can be used to remove excess IgE from blood, and to detect and quantify IgE. This would allow the development of therapy and diagnosis of allergy.
                                                                                                                                                                                                                                                                                                                                              WPI;
                                           AAP81112;
                                                             AAP81112 standard;
                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                         New DNA contg. nucleotide sequence encoding Fc epsilon receptor for obtaining IgE-binding substance used to detect and quantify IgE responsible for allergies.
                                                                                                                                                                                                                                                                                                                                                                                    05-SEP-1986;
24-APR-1987;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              JP63198988-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Fc gamma receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim
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                                                                                                                                                                                                                                                                     Disclosure; ge 529; 16pp; japanese.
                                                                                                                                                                                                                                                                                                                                     N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                   24-APR-1987;
                                                                                                                                                                                                                                                                                                                                                                                                                                         17-AUG-1988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Fc epsilon receptor; IgE; allergy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAP81230;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAP81230 standard; protein; 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                 (KURS ) KURARAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          25-OCT-1990
                                                                                                                 118
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                                                                                                                            ADLSSFKSQEL 11
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DB; AAN81612.
                                                                                                                ADLSSFKSQEL 128
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11; Conserv
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                                                                                                                                                                                                  321 AA;
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                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; ilarity 100.0%; Conservative 0;
                     (first entry)
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87US-0042445.
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                                                             peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        reactions produced by the expression of IgE
                                                                                                                                                                100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    English.
                                                              321
                                                                                                                                                         <u>.</u>.
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                                                                                                                                                        Score 51; DB
Pred. No. 0.1
0; Mismatches
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Pred. No.
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                                                                                                                                                                  DB 9;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 9;
                                                                                                                                                         0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 321;
                                                                                                                                                                          Length 321;
                                                                                                                                                         Indels
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                                                                                                                                                        Gaps
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                                                                                                                                                       0;
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                                                                                                                                                                                                                                       RESULT 9
AAP81172
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                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                  The peptide is related to the IgE receptors on human B-cells and, if without the membrane anchoring sequence, to the IgE-BFs of Sarfati et al. Immunology 53, 197, 207, 783 (1984).

Amino acids between 1-133 starting from the N-terminal may be deleted. This is the membrane-anchoring sequence binding the polypeptide to the cytoplasmic membrane of the B-cells.

Alternatively amino acids between 110-130 or 250-321 may also be deleted. The peptide has IgE binding activity and is useful tor treating allergic conditions, e.g. as caused by antigens such as pollens, cat danders and house dust mites.
11-APR-1987;
21-AUG-1986;
                                                                      EP259615-A.
                                                                                                                                           Sequence encoded by a gene for the water-soluble part of the human low affinity FC-epsilon-receptor with the amino acids 150 to 321, comprising the EcoRI insert from pFC-epsilon-R-1.
                                                                                                                                                                                                           AAP81172;
                                                                                                                                                                                                                             AAP81172 standard;
                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New IgE binding factor related polypeptide(s) - produced by DNA recombinant methods.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1988-022917/04.
N-PSDB; AAN81437.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             22-JUL-1986;
07-NOV-1986;
                              06-AUG-1987;
                                                  16-MAR-1988
                                                                                          Homo sapiens
                                                                                                              therapy.
                                                                                                                                                                                      28-MAR-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20-JUL-1987;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EP254249-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human IgE binding factor; IgE-BFs; allergic diseases; B-cells.
                                                                                                                       Low affinity Fc-epsilon-receptor;
                                                                                                                                                                                                                                                                                 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hofstetter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (CIBA ) CIBA GEIGY AG
                                                                                                                                                                                                                                                                                                    1 ADLSSFKSQEL 11
                                                                                                                                                                                                                                                                                ADLSSFKSQEL 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1; Page 36; 48pp;
                                                                                                                                                                                                                                                                                                                        11;
                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                 321 AA;
                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                     (first entry)
87EP-0105425
86EP-0111581
                              87EP-0111392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Kilchherr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             86GB-0017862
86GB-0026622
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             87EP-0110458
                                                                                                                                                                                                                              Protein; 321
                                                                                                                                                                                                                                                                                                                                  100.0%;
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                                                                                                                                                                                                                                                                                                                         0
                                                                                                                                                                                                                                                                                                                                  Score 51;
Pred. No.
                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                        systemic IgE-allergic reaction;
                                                                                                                                                                                                                                                                                                                                  0.12;
                                                                                                                                                                                                                                                                                                                                            DB 9;
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Gaps

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RESULT 10
AAP90120
ID AAP90
XX
AAP90120
AC AAP9C
XX
DT 01-NC
XX
DE Huma
XX
Huma
KW Huma
KW Huma
KW Homc
XX
FO EP3
XX
PN EP3
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PN EP3
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PN 26-
XX
PF 20-
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PF 30-
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Best Local :
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05-DEC-1986;
06-AUG-1987;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           preparing FCR. Preferred embodiments of the present invention are psfc-epsilon-R-1 (see AAN81516/P81175) and also AAP81172. At least a part of the cDNA SQ coding for the AMS 1 to 148 of the Fc-epsilon-R is replaced by a eucaryotic cDNA signal SQ e.g.an interleukin cDNA signal SQ e.g.by the BSF-2 signal SQ (see pBSF-2-L8-AAN81517/P81176). A suitable yeast expression vector is a plasmid contg. the yeast ADHI-promoter, a gene coding for the yeast mating factor alpha leader peptide (MF alpha leader SQ) a multicloning site and the yeast ADHI-terminator (see AAN81514/P81173). See also EP-258492.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The inventors claim a human low affinity Fc-epsilon-receptor (FCR) with an N-terminal cytoplasmic domain, a C-terminal extracellular domain and a mol.wt. of about 46kd. Also claimed are recombinant DNA conty, the genetic information for the FCR, vectors conty, the DNA, host organisms transformed with the vectors, oligonucleotides coding for partial amino acid sequences from FCR, and processes for
                                                                                                                                                                                                                                                                                                                                    Human lymphocyte receptor
asthma; immunoglobulin E;
                                                                                                                                                                                                                                                                                                                                                                                                                                        01-NOV-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAP90120 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 3; Table 3, Page 79-81; 118pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Recombinant human low affinity Fc(epsilon) - receptor - the treatment of local and systemic IGE-allergic reacti
  WPI; 1989-214148/30
                                                                                                                                          20-JAN-1988;
                                                                                                                                                                              20-JAN-1988;
                                                                                                                                                                                                                       26-JUL-1989
                                                                                                                                                                                                                                                           EP324879-A
                                                                                                                                                                                                                                                                                                Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                             Human lymphocyte receptor for immunoglobulin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAP90120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (OSAU ) OSAKA UNIVERSITY. (KISH/) KISHIMOTO T.
                                          Schwendenwein
                                                            Kishimoto T,
                                                                                                 (OSAU ) OSAKA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  118 ADLSSFKSQEL 128
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        321 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                      Suemura M, Kikutani H, Barsumian R, Sommergruber W, Swetly P;
                                                                                                 UNIVERSITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Suemura M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 86EP-0113073.
86EP-0116938.
87EP-0111392.
                                                                                                                                          88EP-0100814
                                                                                                                                                                              88EP-0100814.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kikutani H,
                                                                                                                                                                                                                                                                                                                                    for immunoglobulin;
lymphocyte receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 51;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ß
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Barsumian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 9;
0.12;
                                                                                                                                                                                                                                                                                                                                                       hypersensitivity; allergy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 321
                                                        EL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      [[
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                          Schneider
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      used
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
                                                                                                                                                                                                                                                   RESULT 12
AAR42053
ID AAR42
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Best
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                                                                     Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Whole human lymphocyte receptor for immunoglobulin (see corresp. AAN90344). Used to produce highly bioactive water-soluble FCR. Water-soluble FCR binds 1gE, so it is useful for treating hypersensitivity, esp. asthma. Amino acid residue 150 is a possible site for trypsin-like proteases.

    used for treatment or prophylaxis of local and
allergic reactions induced by IgE.

                                                                                                                                                                                               Cloned genes coding for soluble IgE receptor - coding sequence of Fc epsilon receptor gene.
                                                                                                                                                                                                                                       WPI; 1989-186101/26.
N-PSDB; AAN90134, AAN90135, AAN90136.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; fig 1; 23pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Soluble recombinant Fc-epsilon receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-PSDB; AAN90344.
                                                                                                                                                                    Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                               EP321601-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Fc epsilon receptor; cloned gene; IgE; allergy; ,asthma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Peptide sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-NOV-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAP90367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAP90367 standard; protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                              Sequence
                                                                                                                                          The known
                                                                                                                                                                                                                                                                                    Kishimoto T,
                                                                                                                                                                                                                                                                                                                                                                       22-DEC-1987;
118
                                                                                                                                                                                                                                                                                                               (OSAU ) OSAKA UNIVERSITY
                                                                                                                                                                                                                                                                                                                                            22-DEC-1987;
                                                                                                                                                                                                                                                                                                                                                                                                   28-JUN-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              118
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                           Н
ADLSSFKSQEL
                          ADLSSFKSQEL
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                                                       11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                        peptide sequence of Fc epsilon receptor gene
                                                                                                               321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           321 AA;
                                                                                                                                                                    fig 1; 19pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first
                                                                                                                                                                                                                                                                                   Suemura M,
                                                                                                               ξ
                                                                                                                                                                                                                                                                                                                                            87EP-0119080
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       mutated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%;
                                                                     100.0%;
                                                                                                                                                                    English.
                                                                                                                                                                                                                                                                                    Kikutani H,
                                                       0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EC
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                                                                   Score 51;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 51;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     epsilon
                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ξ
                                                                                                                                                                                                                                                                                    Barsumian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     receptor
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                                                                   0.12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 10;
                                                                                  BB
                                                                                  10;
                                                       0;
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                                                                                                                                                                                                               comprising modified
                                                                                  Length 321;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 321;
                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                       0;
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                                                       Gaps
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AAR42053 standard; Protein; 321

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RESULT 13
AAW13142
ID AAW13
XX AAW13
XX 17-JU
XX Seque
XX Seque
XX Human
KW Human
KW Lsofo
XX Homo
XX Homo
XX Homo
XX Homo
XX FT Pept1
XX PP900
PN JP090
PP 04-FE
XX 27-DE
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Best Local S
Matches 11
                                                                   Key
Peptide
                                                                                                                    Human; soluble; CD23; complementarity isoform A; recombinant production.
                                                                                                                                                                                                                                                                                                                                                             The sequence is of IgE-binding factor, secreted from the plasmid pSVG-BF. The plasmid pSVG-BF is a derivative of plasmid pSVG-ER which has the sequence coding amino acids 1-147 replaced with a coding region (AAQS5400) allowing secretion of the factor.
                                                                                                                                                                                                                                                                                                                                                                                                                                 Recombinant DNA molecule - comprises enhancer and promoter unit linked to transcriptive DNA segment and DNA segment comprising promoter unit linked to DNA sub-segment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Key
Region
 27-DEC-1995;
                  04-FEB-1997
                                       JP09028385-A
                                                                                                  Homo
                                                                                                                                                  Sequence containing human soluble CD23
                                                                                                                                                                       17-JUN-1997
                                                                                                                                                                                           AAW13142;
                                                                                                                                                                                                             AAW13142 standard; Protein;
                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Page 28; 71pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1993-275121/35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                03-DEC-1987;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    03-DEC-1987;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        08-JUL-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IL84702-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IgE; binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18-FEB-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAR42053;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (CIBA ) CIBA GEIGY AG
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                                                                                                                                                                                                                                                               118
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                                                                                                                                                                                                                                                                                ADLSSFKSQEL 11
                                                                                                  sapiens
                                                                                                                                                                                                                                                               ADLSSFKSQEL 128
                                                                                                                                                                                                                                                                                                    l Similarity
11; Conserv
                                                                                                                                                                                                                                                                                                                                            321 AA;
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illarity 100.
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             factor.
                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         factor;
 95JP-0341169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                87IL-0084702
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    87IL-0084702
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers 148..321 /label= IgE-binding
                                                                   Location/Qualifiers
                                                           /note-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        secretion; expression; signal sequence.
                                                           "soluble CD23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IgE-binding_factor
                                                                                                                                                                                                                                                                                                           .08;
                                                                                                                                                                                                             321
                                                                                                                                                                                                                                                                                                     0;
                                                                                                                                                                                                                                                                                                   Score 51; DB
Pred. No. 0.1
0; Mismatches
                                                                                                                                                                                                             ₹
                                                           isoform
                                                                                                                              determining;
                                                                                                                                                  isoform A.
                                                                                                                                                                                                                                                                                                              DB 14;
0.12;
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                                                                                                                                                                                                                                                                                                    0
                                                                                                                                                                                                                                                                                                                       Length
                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                        321;
                                                                                                                                                                                                                                                                                                   0
                                                                                                                                                                                                                                                                                                   Gaps
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RESULT 14
AAP82839
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Best Local S
Matches 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (LYNC/) LYNCH R G.
(MATS/) MATSUI M.
(NUNE/) NUNEZ R M.
(YODO/) YODOI J.
        This protein is useful in the treatment of local or systemic IgE-allergic reactions and is obtd. By recombinant DNA methods. pref. un-accompanied by associated native glycosylation. Fragit can also be used. See also AAN82253.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The specification states that the nucleotide sequences contained in figures 4a-b, 5a-b, 12a-12b and 13a-b are claimed, however this numbering scheme does not relate to the scheme used in the relevant sections of the specification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DNA sequence encoding a soluble isoform of CD23 scale preparation of the protein % \left\{ 1\right\} =200
                                                                Disclosure; ;
                                                                                     New human low affinity Fc(epsilon)-receptor and parts - useful treating local or systemic IgE-allergic reactions and obtd. by recombinant DNA methods.
                                                                                                                                   WPI; 1988-065440/10.
N-PSDB; AAN82252.
                                                                                                                                                                    Kishimoto T,
                                                                                                                                                                                                                05-DEC-1986;
                                                                                                                                                                                                                                     05-DEC-1986;
                                                                                                                                                                                                                                                          09-MAR-1988.
                                                                                                                                                                                                                                                                                 EP258492-A.
                                                                                                                                                                                                                                                                                                     Fc(epsilon)
                                                                                                                                                                                                                                                                                                                           Human low affinity Fc(epsilon)
                                                                                                                                                                                                                                                                                                                                                                         AAP82839;
                                                                                                                                                                                                                                                                                                                                                                                              AAP82839
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The cDNA encoding the present sequence, soluble CD23 isoform A, can be used for production of soluble CD23.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; Pages 16-17; 33pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1997-159094/15
N-PSDB; AAT61955.
                                                                                                                                                                                                                                                                                                                                                  16-NOV-1990
                                                                                                                                                                                          (CELL-) CELLULAR IMMUNOLOGY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        28-DEC-1994;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADLSSFKSQEL 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              h 100.0%;
Similarity 100.0%;
11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                              standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            321 AA;
                                                                                                                                                                                                                                                                                                      receptor;
                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                рp;
                                                                                                                                                                    Suemura
                                                                                                                                                                                                               86EP-0116938
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        94US-0365103.
                                                                                                                                                                                                                                     86EP-0116938
                                                                English.
                                                                                                                                                                                                                                                                                                                                                                                             protein;
                                                                                                                                                                    Z,
                                                                                                                                                                                                                                                                                                     low affinity; IgE-allergic reactions
                                                                                                                                                                    Kikutani H,
                                                                                                                                                                                                                                                                                                                                                                                               336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 51; DE
Pred. No. 0.1
); Mismatches
                                                                                                                                                                                                                                                                                                                            receptor.
                                                                                                                                                                                                                                                                                                                                                                                               ⋛
                                                                                                                                                                    Barsumian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 18;
0.12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       which contains human the large scale recombinant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0

    useful for large

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                      Fragments
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                  of
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RESULT 15
ABB96396
XX ABB96
XX ABB96
XX ABB96
XX Human
XW Human
XW Gasti
XX Gasti
XX
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Best Local S
Matches 11
    31-JAN-2000;
04-FEB-2000;
24-FEB-2000;
02-MAR-2000;
16-MAR-2000;
17-MAR-2000;
11-JUN-2000;
28-JUN-2000;
29-JUN-2000;
20-JUL-2000;
21-JUL-2000;
21-AUG-2000;
11-AUG-2000;
11-AU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; testicular antigen; testes; cancer; metastasis; immune disorder; reproductive system disorder; urinary system disorder; gene therapy; cardiovascular disorder; respiratory disorder; neurological disorder; gastrointestinal disease; infection; cytostatic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          02-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human testicular antigen SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21-JUN-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 ADLSSFKSQEL 11
|||||||||
8 ADLSSFKSQEL 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              h 100.0%;
Similarity 100.0%;
11; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2000US-0179065.
2000US-0184664.
2000US-0184664.
2000US-0186350.
2000US-0189874.
2000US-0190076.
2000US-0198123.
2000US-0205515.
2000US-0209467.
                     2000US-0214866.
2000US-0215135.
2000US-0216880.
2000US-021487.
2000US-0217487.
2000US-0218296.
2000US-0224518.
2000US-0224518.
2000US-0225214.
2000US-0225214.
2000US-0225266.
2000US-0225266.
2000US-0225267.
2000US-0225268.
2000US-0225277.
2000US-022547.
2000US-022547.
2000US-022547.
2000US-022547.
2000US-02254868.
2000US-02256881.
2000US-02256881.
2000US-0225868.
2000US-02258681.
2000US-02258868.
2000US-0229887.
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      2000US-
2000US-
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2000US-
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2000US-
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Search completed: March 13, 2003, 18:49:13 Job time: 30.2 secs
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Best Local Similarity 80.0%;
Matches 8; Conservative
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01-DEC-2000;
05-DEC-2000;
05-DEC-2000;
05-DEC-2000;
06-DEC-2000;
08-DEC-2000;
                                                                                                                                                                                                                   The present invention provides the protein and coding sequences of 973 human testicular antigens, and fragments of their genomic sequences. The sequences can be used in the treatment of cardiovascular, urinary system, reproductive system, immune, respiratory, neurological and gastrointestinal disorders, infections, and particularly cancer, especially testicular cancers. The present sequence is a protein of the
                                                                                                                                                                                                                                                                                                                                                       Nucleic acids encoding 973 human testicular antigen polypeptides, useful for preventing, diagnosing and/or treating testicular cancer
                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                           Claim 11; SEQ ID NO 1780; 766pp; English.
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34 DLSSFKSGEI 43
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Pred. No. 4.8;
1; Mismatches
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 200000000
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Perfect score:
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US-08-971-317A-6
US-09-131-237-6
US-09-131-237-6
US-09-103-663-6
US-09-103-663-6
US-09-207-287-6
US-09-927-110-1
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2 US-09-927-110-1
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US-09-131-7A-4
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US-09-731-71-35-9
US-09-731-71-35-9
US-09-731-73-35-9
US-09-746-359A-8
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                  Sequence 6, Appli
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Sequence 4, Appli
Sequence 5, Appli
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Sequence 10, Appli
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US-08-971-317A-6
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ALIGNMENTS	US-10-174-590-106	-09	US-09-999-832A-264	US-10-066-500-121	US-09-978-192A-264	US-09-978-697-264	US-09-978-295A-264	US-09-833-435A-9	US-09-764-870-291	US-09-815-242-13624	US-09-815-242-13284	US-09-765-272-172	US-09-771-161A-188	US-09-815-242-13618	US-09-815-242-13365	US-09-933-999A-6	US-09-771-161A-97	US-09-801-368-346	US-09-815-242-13646	US-09-841-739-11	US-09-738-626-6798	US-09-886-241-6	us-09-867-550-686	US-10-007-693-73	US-09-841-132-523	5
	106,	264	264,	Sequence 121, App	264,	264,	264		29	13	13284		188,		Sequence 13365, A	6, AF	97, 7	Sequence 346, App	1364	11,	6798	Sequence 6, Appli	88	73, /	Sequence 523, App	Sequence 10, Appl

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GENERAL INFORMATION:
APPLICANT: Wiley, Steven R.
TITLE OF INVENTION: THE BOT
TITLE OF INVENTION: THEREOF
NUMBER OF SEQUENCES: 10
                                                                                                                             APPLICATION NUMBER: US/08/971
FILING DATE: 17-NOV-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: GOller, Mimic
REFERENCE/DOCKET NUMBER: 6255
TELECOMMUNICATION INFORMATION:
TELEPHONE: (847) 935-7550
TELEFAX: (847) 938-2623
                                                                                               INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                               OPERATING SYSTEM: Windows
SOFTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
ADDRESSEE: Abbott Laboratories
STREET: 100 Abbott Park Road
CITY: Abbott Park
                                     SEQUENCE CHARACTERISTICS:
LENGTH: 281 amino acids
TYPE: amino acid
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER:
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CURRENT APPLICATION NUMBER: US/09/131,237B
CURRENT FILING DATE: 1998-08-07
EARLIER APPLICATION NUMBER: 60/074,047
EARLIER FILING DATE: 1998-02-09
EARLIER FILING DATE: 1998-01-09
EARLIER FILING DATE: 1998-01-09
EARLIER FILING DATE: 1998-01-09
EARLIER APPLICATION NUMBER: 08/461,246
EARLIER APPLICATION NUMBER: PCT/US94/12880
EARLIER APPLICATION NUMBER: PCT/US94/12880
EARLIER FILING DATE: 1994-11-07
NUMBER OF SEO ID NOS: 24
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Matches
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Best Local Similarity 100.
Matches 11; Conservative
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SEQ ID NO 6
LENGTH: 281
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APPLICANT: N1, Jian
APPLICANT: ROSen, Craig A.
TITLE OF INVENTION: Tumor Necrosis Factor Gamma
FILE REFERENCE: PF141P3
                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
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Local Similarity 100.0%;
see 11; Conservative (
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   COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 Diskette
COMPUTER: IBM FC computible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSE: Pharmacia & Upjohn, Intellectual Property
                                                                                                                                                                                                                                                                                 Mills, Cynthia J
Jones, David A
TITLE OF INVENTION: TNF-Related Death Ligand
                                                                                                                                                                                                                                                                                                                                           APPLICANT: Bienkowski, Michael J
                                                                                                                                                                        STREET: 301 Henrietta Street CITY: Kalamazoo
                                                                                                                                      COUNTRY: USA
                                                                                                                                                         STATE: MI
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Pred. No.
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                        Version #1.25
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APPLICANT: Wiley, Steven R.
TITLE OF INVENTION: TNR-DELTA LIGAND AND USES THEREOF FILE REFERENCE: 6255,US.02
CURRENT APPLICATION NUMBER: US/09/193,663
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US-09-193-663-6
                                                                               RESULT 5
                                                                                                                                                                                                                                                                                     ; ORGANISM: Homo sapiens US-09-802-669-25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; MOLECULE TYPE: protein ; SEQUENCE DESCRIPTION: SEQ ID US-10-174-654-10
                                                                                                                                                                                              Query Match
Best Local Similarity 100.
Matches 11; Conservative
Sequence 6, Application US/09193663
Patent No. US20020055624A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: PatentIn Ver. 2.0 SEQ ID NO 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
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Best Local Similarity 100.0%;
Matches 11; Conservative
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APPLICANT: Marcusson, Eric G.
APPLICANT: Wyatt, Jacqueline
APPLICANT: Zhang, Hong
TITLE OF INVENTION: Antisense Compound Modulation of Fas Mediated Signaling
FILE REFERENCE: ISPH-545
CURRENT APPLICATION NUMBER: US/09/802,669
CURRENT FILING DATE: 2001-03-09
PRIOR APPLICATION NUMBER: US 09/665,615
PRIOR APPLICATION NUMBER: US 09/665,615
PRIOR FILING DATE: 2000-09-18
PRIOR FILING DATE: 1909-04-12
NUMBER OF SEO ID NOS: 180
PRIOR SECULORY NUMBER: US 09/290,640
                                                                                                                                                                                                                                                                                                                          LENGTH: 28
TYPE: PRT
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INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 281 amino acids
TYPE: amino acid
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109 KELAELRESTS 119
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FILING DATE: 19-Jun-2002
CLASSIFICATION: CUMKNOWN>
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                             281
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REGISTRATION NUMBER: 41,113
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                                                                                                                                                                                                                             100.0%; Score 50; 100.0%; Pred. No.
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Pred. No. 0.0
0; Mismatches
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GENERAL INFORMATION:

APPLICANT: Ebner, Reinhard

APPLICANT: Ruben, Steven M.

APPLICANT: Ulitich, Stephen

TITLE OF INVENTION: Apoptosis Inducing Molecule II

FILE REFERENCE: 1488.0650004

CURRENT APPLICATION NUMBER: US/09/027,287A

CURRENT FILING DATE: 1998-02-20

EARLIER APPLICATION NUMBER: US 09/003,886

EARLIER APPLICATION NUMBER: US 08/822,953

EARLIER APPLICATION NUMBER: US 60/030,157

EARLIER APPLICATION NUMBER: US 60/030,157

EARLIER FILING DATE: 1996-10-31

EARLIER FILING DATE: 1996-10-31

EARLIER FILING DATE: 1996-03-22

NUMBER: US 60/013,923
                                                                                                         Sequence 6, Application US/09252656B
Patent No. US20020081647A1
GENERAL INFORMATION:
APPLICANT: Ebner, Reinhard
APPLICANT: Yu, Guo-Liang
APPLICANT: Ruben, Steven M.
APPLICANT: Zhang, Jun
APPLICANT: Thing, Jun
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; SOFTWARE: FastSEQ for Windows Version 3.0; SEQ ID NO 6; LENCTH: 281
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-193-663-6
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US-09-027-287-6
                                                                                                                                                                                                                                               US-09-252-656B-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 6
LENGTH: 281
                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
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Best Local Similarity
TITLE OF INVENTION: Apoptosis Inducing Molecule II and Methods of FILE REFERENCE: 1488.0650006 CURRENT APPLICATION NUMBER: US/09/252,656B CURRENT FILING DATE: 1999-02-19
                                                                          APPLICANT: Zhang, Jun
APPLICANT: Ullrich, Stephen
APPLICANT: Zhai, Yifan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT FILING DATE: 1998-11-17 EARLIER APPLICATION NUMBER: 60/
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Pred. No.
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Pred. No.
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; LENGTH: 281; TYPE: PRT; ORGANISM: Homo sapiens; FEATURE: FEATURE: OTHER INFORMATION: Description of Combined DNA/RNA Molecule: n equals; OTHER INFORMATION: a, t, g, or c US-09-929-493-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; TYPE: PRT ; ORGANISM: Homo sapiens US-09-252-656B-6
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Best Local Similarity
Matches 11; Conserv
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    Matches
                    Query Match
Best Local Similarity
                                                                                                                                                                                                                     SEQ ID NO 6
                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: 60/234,338
PRIOR FILING DATE: 2000-09-22
PRIOR APPLICATION NUMBER: 60/240,806
PRIOR FILING DATE: 2000-10-17
PRIOR PRIOR FILING DATE: 2000-11-30
PRIOR FILING DATE: 2000-11-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT FILING DATE: 2001-08-15
PRIOR APPLICATION NUMBER: 60/225,628
PRIOR FILING DATE: 2000-08-15
PRIOR APPLICATION NUMBER: 60/227,008
PRIOR FILING DATE: 2000-08-23
PRIOR FILING DATE: 2000-08-23
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PRIOR FILING DATE: 1996-03-22
PRIOR APPLICATION NUMBER: US 60/030,157
PRIOR FILING DATE: 1996-10-31
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CURRENT FILING DATE: 2001-08-15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: Neutrokine-alpha and Neutrokine-alpha Splice Variant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Yu et
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: PatentIn version 3.1
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PRIOR FILING DATE: 1998-02-20
PRIOR APPLICATION NUMBER: US 09/003, 886
PRIOR FILING DATE: 1998-01-07
PRIOR APPLICATION NUMBER: US 08/822, 953
PRIOR FILING DATE: 1997-03-21
                                                                                                                                                                                                                                        SOFTWARE: Patentin
                                                                                                                                                                                                                                                             NUMBER OF SEQ ID NOS: 47
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                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: 60/
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FILING DATE: 2001-03-06
APPLICATION NUMBER: 60/293,499
FILING DATE: 2001-05-25
                                                                                                                                                                                                                                                                               FILING DATE:
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                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: 60/296,122
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    Conservative
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Pred. No. 0.051;
                    Score 50; DB 10
Pred. No. 0.051;
    Mismatches
                                       10;
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1 KELAELRESTS 11

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NUMBER OF SEQ ID NOS: 1
SOFTWARE: PatentIn version 3.0
SEQ ID NO 1
LENGTH: 281
TYPE: PAT
ORGANISM: Homo sapiens
US-09-927-110-1
                                                                                                                                                                                                                   ; SOFTWARE: Patentin Ver. 2
; SEO ID NO 13
; LENGTH: 281
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-012-452-13
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RESULT 11
US-09-246-129B-6
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Best Local Similarity 100.
Matches 11; Conservative
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APPLICANT: SEABRIGHT CORPORATION LIMITED
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                                                                                                                                                 Matches
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Best Local (
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Patent No. US20020111325A1
                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/10/012,452 CURRENT FILING DATE: 2001-12-12 PRIOR APPLICATION NUMBER: 09/559,290 PRIOR FILING DATE: 2000-04-27 PRIOR APPLICATION NUMBER: PCT/US98/23191 PRIOR FILING DATE: 1998-11-02 PRIOR APPLICATION NUMBER: 08/963,272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: LI, et al. TITLE OF INVENTION: VEGI, An Inhibitor of Angiogenesis and Tumor Growth FILE REFERENCE: PF141P5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: PATY, Donald
APPLICANT: LUO, Liqing
TITLE OF INVENTION: METHOD FOR INHIBITING INFLAMMATION IN IMMUNE PRIVILEGED SITES USI
TITLE OF INVENTION: LIGAND FRAGMENTS
FILE REFERENCE: MBM1240
                                                                                                                                                                                                                                                                                                                             PRIOR FILING DATE: 1997-11-03
NUMBER OF SEQ ID NOS: 31
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CURRENT FILING DATE: 2001-08-10
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PRIOR FILING DATE: 2000-08-10
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                                                                       109 KELAELRESTS 119
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CYNADER, Max
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Pred. No. 0.051;
; Mismatches 0;
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Pred. No. 0.051;
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APPLICANT: Ni, Jian

APPLICANT: ROSED, Craig A.

TITLE OF INVENTION: TUMOZ NECROSIS FACTOR Gamma

FILE REFERENCE: PF141P4

CURRENT APPLICATION NUMBER: US/09/246,129B

CURRENT FILING DATE: 1999-02-08

PRIOR APPLICATION NUMBER: 60/074,047

PRIOR FILING DATE: 1998-02-09

PRIOR APPLICATION NUMBER: 09/131,237

PRIOR FILING DATE: 1998-08-07

PRIOR FILING DATE: 1998-08-07

PRIOR FILING DATE: 1998-01-09

PRIOR FILING DATE: 1998-01-09

PRIOR APPLICATION NUMBER: 09/05,020

PRIOR FILING DATE: 1998-01-09

PRIOR APPLICATION NUMBER: 08/461,246

PRIOR FILING DATE: 1995-06-05

PRIOR FILING DATE: 1995-06-05
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                                     PRIOR APPLICATION NUMBER: 60/216,879
PRIOR FILING DATE: 2001-03-26
PRIOR APPLICATION NUMBER: 60/216,879
PRIOR FILING DATE: 2000-07-07
PRIOR PELICATION NUMBER: 09/559,290
PRIOR APPLICATION NUMBER: 09/559,290
PRIOR FILING DATE: 2000-04-27
PRIOR APPLICATION NUMBER: 60/180,908
PRIOR APPLICATION NUMBER: 60/134,067
PRIOR APPLICATION NUMBER: 60/134,227
PRIOR APPLICATION NUMBER: 60/132,227
PRIOR APPLICATION NUMBER: 60/131,237
PRIOR APPLICATION NUMBER: 60/131,963
PRIOR APPLICATION NUMBER: 09/246,129
PRIOR APPLICATION NUMBER: 09/246,129
PRIOR APPLICATION NUMBER: 09/04-04
PRIOR APPLICATION NUMBER: 09/04,047
PRIOR APPLICATION NUMBER: 09/04,047
PRIOR APPLICATION NUMBER: 09/04,047
PRIOR APPLICATION NUMBER: 09/04,047
PRIOR APPLICATION NUMBER: 09/131,237
PRIOR FILING DATE: 1998-02-09
PRIOR APPLICATION NUMBER: 09/131,237
PRIOR FILING DATE: 1998-03-07
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; LENGTH: 278
; TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILE REFERENCE: PF141P7
CURRENT APPLICATION NUMBER: US/09/899,059
CURRENT FILING DATE: 2001-07-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
                       PRIOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR FILING DATE: 1994-11-07
NUMBER OF SEQ ID NOS: 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Rattus norvegicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ITLE OF INVENTION: Tumor Necrosis Factor Gamma
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APPLICATION NUMBER: 09/005,020 FILING DATE: 1998-01-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6, Application US/09246129B
o. US20020090683A1
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Zhang, Jun
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PRIOR FILING DATE: 1995-06-05

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RESULT 13
US-08-971-317A-4
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LENGTH: 278
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Best Local :
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Best Local
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PRIOR FILING DATE: 1994-11-07
NUMBER OF SEQ ID NOS: 30
SOFTWARE: Patentin Ver. 2.0
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GENERAL INFORMATION:
                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: 4: SEQUENCE CHARACTERISTICS: LENGTH: 279 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows
SOFTWARE: FASKEED for Windows Version 2.0b
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                       NAME: Goller, Mimi C
REGISTRATION NUMBER: 39,046
REFERENCE/DOCKET NUMBER: 6255.US.01
TELECOMMUNICATION INFORMATION:
TELEPHONE: (847) 935-7550
TELEPAX: (847) 938-2623
                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
ATTORNEY/AGENT INFORMATION:
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CORRESPONDENCE ADDRESS:
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TITLE OF INVENTION: THE DELTA LIGAND AND USES
TITLE OF INVENTION: THEREOF
                                                                                                                                               MOLECULE TYPE:
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Local Similarity 81.8%;
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KELAELREFTN 117
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Pred. No. 2.
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Pred. No.
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ORGANISM: MUS musculus ; SEQUENCE DESCRIPTION: SEQ ID NO: 5: US-10-017-910-5
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US-09-193-663-4
                                                                          GENERAL INFORMATION: APPLICANT: Wiley, S
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                                                                                                             Sequence 4, Application US/09193663 Patent No. US20020055624A1
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TITLE OF INVENTION: THE DELTA LIGAND AND USES THEREOF FILE REFERENCE: 6255.US.02
CURRENT APPLICATION NUMBER: US/09/193,663
CURRENT FILING DATE: 1998-11-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEX: 133521
INFORMATION FOR SEO ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 279 amino acids
TYPE: amino acid
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TITLE OF INVENTION: A PROTEIN BELONGING TO THE THE SUPERFAMILY
INVOLVED IN SIGNAL TRANSDUCTION, NUCLEIC ACMETHODS OF USE THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC COMPATIBLE

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PATENTIN Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/017,910

FILING DATE: 14-Dec-2001

CLASSIFICATION: <UNknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US 09/447,035
FILING DATE: 1999-11-22
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: protein HYPOTHETICAL: NO ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION: TELEPHONE: 201-487-5800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
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ADDRESSEE: Klauber & Jackson
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                                                                                                                                                                                                                                KELAELREFTN 117
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STATE: New Jersey
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                                                                          Steven R
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## CARLIER APPLICATION NUMBER: 60/065,916
### CARLIER FILING DATE: 1997-11-17
### NUMBER OF SEQ ID NOS: 10
### SEQ ID NOS: 10
### SEQ ID NOS: 10
### SEQ ID NO 4
### SEQ ID NO 5
### SEQ ID NO 4
### SEQ ID NO 5
### SEQ ID NO 5
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### SEQ ID NO 5
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Result
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Maximum DB seq length: 200000000
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Match Length DB
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/cgn2_6/ptodata/2/1aa/5B_COMB.pep:*
/cgn2_6/ptodata/2/1aa/6A_COMB.pep:*
/cgn2_6/ptodata/2/1aa/6B_COMB.pep:*
/cgn2_6/ptodata/2/1aa/6B_COMB.pep:*
/cgn2_6/ptodata/2/1aa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/2/1aa/backfiles1.pep:*
                                                                         US-08-649-100-9 . US-08-810-453-214-6 . US-08-815-190A-2 . US-08-815-190A-2 . US-08-815-190A-2 . US-08-815-190A-3 . US-08-815-190A-16 . US-08-815-190A-16 . US-08-815-190A-16 . US-08-815-190A-16 . US-08-815-190A-16 . US-08-815-190A-16 . US-08-339-214-14 . US-08-339-214-26 . US-08-339-214-27 . US-08-339-214-27 . US-08-339-214-27 . US-08-339-214-32 . US-08-339-214-32 . US-08-65-08-339-214-32 . US-08-65-08-339-214-34 . US-08-65-08-339-214-32 . US-08-65-08-339-32 . US-08-65-08-339-32 . US-08-65-08-339-32 . US-08-65-08-339-32 . US-08-65-08-339-32 . US-08-65-08-339-32 . US-08-65-08-339-3
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Sequence 9, Appli
Sequence 6, Appli
Sequence 2, Appli
Sequence 2, Appli
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74, Appl
5185254
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3, Appli
30, Appli
6, Appli
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US-08-339-214-84
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   Query Match
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31	31	31	31	31	31	31	31	31	31	31	31	31	31	31	31	31	31
62.0	62.0	62.0	62.0	62.0	62.0	62.0	62.0	62.0	62.0	62.0	62.0	62.0	62.0	62.0	62.0	62.0	62.0
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•	Sequence 23, Appl	Sequence 9, Appli	Sequence 172, App	'n	Sequence 4, Appli	Sequence 5, Appli	Sequence 4, Appli	Sequence 5, Appli	Sequence 4, Appli	Sequence 30, Appl	Sequence 3, Appli	Sequence 3, Appli	Sequence 3, Appli	Sequence 298, App	Sequence 300, App	`	Sequence 276, App

ALIGNMENTS

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; NAME/KEY: Protein
; LOCATION: 1..178
; OTHER INFORMATION:
US-08-339-214-84
                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS_MS-DOS
SOFTWARE: Patentin Release #1.0, Ve.
SOFTWARE: Patentin Release #1.0, Ve.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/339,214
FILING DATE: 10-NOV-1994
CLASSIFICATION: 435
ATTORNEY_AGENT INFORMATION:
NAME: Murphy Jr., Gerald M.
REGISTRATION NUMBER: 28,977
REFERENCE_DOCKET NUMBER: 1110-139P
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-205-8000
                                                                                                                                                                                                                           TELEFAX: 703-205-8050 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
                                                                             MOLECULE TYPE: FRAGMENT TYPE: FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: A Fas Ligand, A Fragment Thereof and TITLE OF INVENTION: Encoding the Same NUMBER OF SEQUENCES: 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
                                                                                                                                         TYPE: amino acid
STRANDEDNESS: not
TOPOLOGY: not rei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: P.O. Box 7.
CITY: Falls Church
STATE: Virginia
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                                                                                                                                                                                                      178 amino acids
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Nakamura, No. 6348334io
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                                                                                                     internal
                                                                                                                          protein
                                                                                                                                                                 not relevant
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                 /note= "polypeptide CD179"
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100.0%;

Score 50;

DB 4; Length 178;

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COMPUTER REDABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION UMBER: US/08/649,100
FILLING DATE:
CLASSIFICATION: 435
ATTONNEY/AGENT INFORMATION:
NAME: MURPHY JR, GERALD M
REGISTRATION NUMBER: 28,977
REPERENCE/DOCKET NUMBER: 1110-160
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 205-8000
TELEFAX: (703) 205-8000
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 179 smino acids
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US-08-339-214-6
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                                                                                                          Sequence 6, Application US/08339214
Patent No. 6348334
GENERAL INFORMATION:
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Best Local Similarity
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APPLICANT:
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APPLICANT:
TITLE OF INV
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CORRESPONDENCE ADDRESS:
ADDRESSE: BIRCH, STEWART, KOLASCH AND BIRCH
STREET: PO BOX 747
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: VASQUEZ, MAXIMILIANO TITLE OF INVENTION: ANTI-FAS LIGAND ANTIBODY AND ASSAY TITLE OF INVENTION: METHOD USING THE ANTI-FAS LIGAND A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: USA
ZIP: 22040-0747
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CITY: FALLS CHURCH
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                T: Nagata, Shigikazu
T: Suda, Takashi
T: Takahashi, Tomoniro
T: Nakamura, No. 634833410
INVENTION: A Fas Ligand, A
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NAGATA, SHIGEKAZU
CO, MAN SUNG
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A Fas Ligand, A Fr
Encoding the Same
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); Mismatches 0;
                    A Fragment Thereof and DNA
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US-08-810-453-2
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Best Local S
Matches 11
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INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 179 amino acids
ATTORNEY/AGENT INFORMATION:
NAME: Plumer, Elizabeth R.
REGISTRATION NUMBER: 36,637
REFERENCE/DOCKET NUMBER: $1237/7004
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)720-3500
TELEPAX: (617)720-2441
                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/810,453
                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wolf, Greenfield & Sacks, P.C.
STREET: Federal Reserve Plaza, 600 Atlantic Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: FAS LIGAND COMPOSITIONS FOR TREATMENT OF TITLE OF INVENTION: PROLIFERATIVE DISORDERS
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TOPOLOGY: linear
                                                                                                                                                                                                                                                                                         COUNTRY: US
ZIP: 02210-2211
                                                                                                                           CLASSIFICATION:
                                                                                                                                               FILING DATE:
                                                                                                                                                                                                                                                                                                                              STATE:
                                                                                                                                                                                                                                                                                                                                                 CITY:
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ZIP: 22040-0747
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: P.O. Box 7
CITY: Falls Church
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                                                                                                                                                                                                                                                                                                                                             Boston
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APPLICATION NUMBER: US/08/339,214
FILING DATE: 10-NOV-1994
CLASSIFICATION: 435
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MUIPHY Jr., Gerald M.
REGISTRATION NUMBER: 28,977
REFERENCE/DOCKET NUMBER: 1110-139P
TELEPHONE: 703-205-8000
TELEPHONE: 703-205-8000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: EIM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIAN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
Match 100.0%; Score 50; DB 4; Local Similarity 100.0%; Pred. No. 0.037; es 11; Conservative 0; Mismatches
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O. Box 747
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Best Local (
                                                                                            Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                                                                                                         TELEFAX: (415) 576-03 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC COMPATIBLE

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PATENTIN Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/815,190A

FILLING DATE: 11-MAR-1997

CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Queen, Cary L.
APPLICANT: Schneider, William P.
APPLICANT: Vasquez, Maximiliano
                                                                                                                                      TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 281 amino acid
                                                                                                                                                                                                                                                                       NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 011823-006710US
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                     FILING DATE: 13-MAR-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES:
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nes 11; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: San Francisco
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                                                                                                                                                                                                                                                         TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US 08/614,584
                                                              Local Similarity es 11; Conserv
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                            1 KELAELRESTS 11
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                                                                                                                                                                                       281 amino acids
                                                           100.0%;
ilarity 100.0%;
Conservative
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Schneider, William P.
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(larity 100.0%;
Conservative 0
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Pred. No. 0.059;
                                                           Score 50; DB 3; Pred. No. 0.059; Mismatches
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                                                                                            DB 3;
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RESULT 6

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; LENGTH: 281
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-290-640-25
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-479-524-3
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US-08-339-214-8
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APPLICANT: Marcusson, Eric G.
TITLE OF INVENTION: Antisense Compound Modulation of Fas Mediated Signaling
FILE REPERENCE: ISPH-0351
CURRENT APPLICATION NUMBER: US/09/290,640
CURRENT FILING DATE: 1999-04-12
NUMBER OF SEQ ID NOS: 85
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Wordperfect
SEQ ID NO 3
LENGTH: 281
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Patent No. 6288350
GENERAL INFORMATION:
APPLICANT: Barbera-Guillem, Emilio
                                                                                                                                                             Sequence 8, Patent No. 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                  Matches
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Best Local Similarity
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CURRENT APPLICATION NUMBER: US/09/479,524

CURRENT FILING DATE: 2000-01-07

EARLIER APPLICATION NUMBER: US 09/170,948

EARLIER FILING DATE: 1998-10-13

EARLIER FILING DATE: 1998-10-13

EARLIER APPLICATION NUMBER: US 60/062,733

EARLIER FILING DATE: 1997-10-23

NUMBER OF SEQ ID NOS: 8
                                                                                                                                                 GENERAL INFORMATION:
                                                                            APPLICANT:
APPLICANT:
APPLICANT:
          TITLE OF INVENTION: A
TITLE OF INVENTION: En
NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
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nes 11; Conserv
ADDRESSEE:
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                                                                                                                                                                             Application US/08339214
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                                                                              Takahashi, Tomoniro
Nakamura, No. 634833410
                                                                                                             Nagata, Shigikazu
Suda, Takashi
                                                                                                                                                                                                                                                                                                                                  Conservative
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Encoding the Same
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Stewart, Kolasch & Birch
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Pred. No.
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Pred. No. 0.059;
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COUNTRY: USA ZIP: 22040-0747

Falls Church Virginia

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US-08-339-214-30
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TELEFAX: 703-200 ES:
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 281 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
               APPLICATION NUMBER: US/08/339,214
FILING DATE: 10-NOV-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Murphy Jr., Gerald M.
REGISTRATION NUMBER: 28,977
REFERENCE/DOCKET NUMBER: 1110-139P
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-205-8000
                                                                                                                                       ZIP: 22040 COMPUTER READBLE FORM:
COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PAtentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
CURRENT APPLICATION NUMBER: US/08/339,214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/339,214
FILING DATE: 10-NOV-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: MULPH Jr., Gerald M.
REGISTRATION NUMBER: 28,977
REFERENCE/DOCKET NUMBER: 1110-139P
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-205-8000
TELEFAX: 703-205-8050
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MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT:
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CITY: Falls Church
STAFE: Virgin's
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity es 11; Conserv
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22040-0747
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Nakamura, No. 6348334io
703-205-8050
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Pred. No. 0.059;
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US-09-157-864-10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQ ID NO 6
LENGTH: 281
TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                              Sequence 10, Application US/09157864
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Matches 11; Conserva
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Best Local Similarity
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TITLE OF INVENTION: Antibodies to Neutrokine-alpha
FILE REFERENCE: PF343P3C1
CURRENT APPLICATION NUMBER: US/09/589, 287B
CURRENT FILING DATE: 2000-06-08
                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Prior application data removed check PALM or file wrapper NUMBER OF SEQ ID NOS: 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: PatentIn Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Homo sapiens
                            COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 Diskette
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURE:
                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                        APPLICANT: Bienkowski, Miche APPLICANT: Mills, Cynthia J APPLICANT: Jones, David A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 281 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                          TITLE OF INVENTION: NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    109 KELAELRESTS 119
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FILING DATE:
              APPLICATION NUMBER:
                                                                                                                                                COUNTRY:
                                                                                                                                                                       STATE:
                                                                                                                                                                                                                    ADDRESSEE: Pharmacia & Upjohn, Intellectual Property
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 KELAELRESTS 11
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                                                                                                                                                                                    Kalamazoo
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301 Henrietta Street
                                                                                                                                                    USA
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                                                                                                                                                                                                                                                                                                                                              Bienkowski, Michael J
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              US/09/157,864
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Pred. No.
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ATTORNEY/AGENT INFORMATION:

Kerber,

CLASSIFICATION:

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; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-157-864-10
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                                                  RESULT 13
PCT-US95-00362-2
                                                                                                                                                                                                                                                            ; OTHER INFORMATION: human wild-type Fas ligand (FasL)
US-09-006-755B-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-006-755B-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Stock, Peter G.
APPLICANT: The Regents of the University of California APPLICANT: The Regents of the University of California TITLE OF INVENTION: A NO. 6451759cleavable Fas Ligand FILE REFERENCE: 18602K-000500US
CURRENT APPLICATION NUMBER: US/09/006,755B
CURRENT FILING DATE: 1998-01-14
NUMBER OF SEQ ID NOS: 12
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 1
                Sequence 2, Application PC/TUS9500362 GENERAL INFORMATION:
                                                                                                                                                                                      Query Match 100.0%; Score 50; D
Best Local Similarity 100.0%; Pred. No. 0.
Matches 11; Conservative 0; Mismatches
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APPLICANT: Braat, Andries E
APPLICANT: Baekkeskov, Steinunn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: DOMAIN
LOCATION: (103)..(281)
OTHER INFORMATION: extracellular domain
                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
                                                                                                                                                                                                                                                                                                         LOCATION: (119)..(154)
OTHER INFORMATION: metalloprotease recognition region
                                                                                                                                                                                                                                                                                                                                             NAME/KEY: PEPTIDE
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 APPLICANT:
                                                                                                                       109
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                                                                                                                                           1 KELAELRESTS 11
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linear
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IMMUNEX CORPORATION
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Tori L.
TORER: 41,113
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Pred. No. 0.059;
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US-08-815-190A-16
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Best Local :
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APPLICATION NUMBER: US 08,
FILING DATE: 07-JAN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08,
FILING DATE: 01-FEB-1994
                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: HBM PC Computible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                      SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/815,190A
                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Queen, Cary L.
APPLICANT: Schneider, William P.
APPLICANT: Vasquez, Maximiliano
APPLICANT: Vasquez, Ese 11 cand 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: Anderson, Kathryn A.
REGISTRATION NUMBER: 32,17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OPERATING SYSTEM: Apple 7.1 SOFTWARE: Microsoft Word, V. CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: Fas Ligand Fusion Proteins and Their TITLE OF INVENTION: Uses
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PRIOR APPLICATION DATA:
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STREET: Seattle
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: Ligand That Binds Fas Antigen
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy disk COMPUTER: Apple Macintosh OPERATING SYSTEM: Apple 7
                                                                                                                                                                                                                         STREET: Two Embarcac
CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: FILING DATE: 06-JAN
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                      CLASSIFICATION:
                                                                                                                                                                                                           COUNTRY: USA
                                      FILING DATE:
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Schneider, William P.
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06-JAN-1995
                                    11-MAR-1997
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COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOUTWARE: PATENTION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/08/751,512
FILING DATE: 15-NOV-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MUTPHY, MATCHEW B.
REGISTRATION NUMBER: 39,787
REFERENCE/DOCKET NUMBER: 02307K-07100US
TELEFOMMUNICATION NUMBER: 0300
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 376 amino acids
TYPE: omino acids
TYPE: omino acids
TYPE: omino acids
TYPE: protein
US-08-751-512-8
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REGISTRATION NUMBER: 36,429

REFERENCE/DOCKET NUMBER: 011823-006710US

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 576-0200

INFORMATION FOR SEQ ID NO: 16:

SEQUENCE CHARACTERISTICS:

LENGTH: 287 amino acids

TYPE: mollocar

MOLECULE TYPE: protein

US-08-815-190A-16
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APPLICANT: Ramer, J. Kevin
APPLICANT: Williams, Lewis T.
TITLE OF INVENTION: Modified FAS Ligands
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 15
US-08-751-512-8
: Sequence 8, Application US/08751512
: Patent No. 6001962
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                                                                          Query Match 100.0%; Score 50; DB 3; Best Local Similarity 100.0%; Pred. No. 0.079; Matches 11; Conservative 0; Mismatches 0
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Best Local Similarity 100.0%;
Matches 11; Conservative 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STATE: CA
COUNTRY: USA
204
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KELAELRESTS 214
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Search completed: March 13, 2003, 18:53:50 Job time: 10.8 secs

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Maximum Match 100%
Listing first 45 summaries
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is derived by analysis of the total score distribution.

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MT16_EMENI
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VIE2_NPVOP
YRG5_CAEEL
YVCE_BACSU
YO65_CHLPN
DARK_MYXXA
CARB_AGRT9
RL29_CHLMU
YMC6_BACSU
YMC6_BACSU
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1 bacillus su
3 human adeno
9 emericella
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1 orgyia pseu
6 caenorhabdi
7 bacillus su
6 chlamydia p
                     7 aquifex aeo
7 methanobact
7 bacillus su
1 populus kit
0 homo sapien
8 bos taurus
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TWF6_CERTO STANDARD; PRT; 280 AA.

ID TNF6_CERTO STANDARD; PRT; 280 AA.

AC O9BDN1;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Tumor necrosis factor ligand superfamily member 6 (FAS antigen ligand)
DE (CD95L protein).
GN TWRSF6 OR FASL OR CD95L.
GN TWRSF6 OR FASL OR CD95L.
OS Cercocebus torquatus atys (Red-crowned mangabey) (Sooty mangabey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutherab; Catarrhini; Cercopithecidae;
CC Cercopithecinae; Cercocebus.
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	P24809 bacillus su					P00961 escherichia				007310 rhodobacter	029048 archaeoglob

ALIGNMENTS

	DR DR
ProDom; PD002012; TNE_Abc; 1.	DR PR
Pfam; pF00229; TNF; 1.	DR DR
InterPro; IPR000478; TNF_family.	DR :
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rnis Swiss-PROT entry is copyright. It is produced through a collaboration - between the Swiss Institute of Bioinformatics and the EMBL outstation -	88
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T cells, or both. Binding to the decoy receptor TNFRSF6B/DcR3	റ്റ
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Immunogenetics	R.
y molecules.";	R.T
"Cloning, sequencing, and homology analysis of nonhuman primate	RΤ
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Villinger F., Bostik P., Mayne A.E., King C.L., Genain C.P.,	₽:
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CARBOHYD
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MRISTE OR FASL OR CD95L.

Macaca mulatta (Rhesus macaque),

Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey), and

Macaca nemestrina (Pig-talled macaque),

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
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                                                                                                                                                                                                                                                             SPECIES-M.mulatta; TISSUE-Lymphocytes; MEDLINE-21383618; pubMed-11491535; VIII109er F., Bostik P., Mayne A.E., King C.L., Weiss W.R., Ansari A.A.; Monology analysis of r"Cloning, sequencing, and homology analysis of r Fas/Fas-11gand and co-stimulatory molecules."; immunogenetics 53:315-328(2001).
                                                                                                                                                                                                                                                                                                                                                                                Cercopithecinae;
NCBI_TaxID-9544,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Tumor necrosis factor ligand superfamily member 6
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Q9MYL6; Q9BDM5;
15-JUN-2002 (Re
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                                                                   transduces the apoptotic signal into cells, May be involved in cytotoxic T cell mediated apoptosis and in T cell development. TNFRSF6/FAS-mediated apoptosis may have a role in the induction of peripheral tolerance, in the antigen-stimulated suicide of mature T cells, or both. Binding to the decoy receptor TNFRSF6B/DCR3 modulates its effects (By similarity).

SUBCELLULAR LOCATION: Type II membrane protein and secretad 'By similarity'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             \vdash
                       PTM: The soluble form derives from the membrane form by proteolytic processing (By similarity).
SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
                                                                 similarity).
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 SWISS-PROT
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TUMOR NECROSIS FACTOR LIGAND SUPERFAMILY
MEMBER 6, MEMBRANE FORM.
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729EA60067B7D398 CRC64;
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SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
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Pred. No. 0.032;
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pfam; pF00229; TNF; 1.

pfam; pF00229; TNF; 1.

prints; pR01234; TNECROSISECT.

proDom; pD002012; TNF_abc; 1.

SMART; SM00207; TNF; 1.

SMART; SM00207; TNF, 1; 1.

PROSITE; pS00251; TNF_1; 1.

PROSITE; pS50049; TNF_2; 1.

TUMOR NECROSIS FACTOR LIGAND SUPERF
TUMOR NECROSIS FACTOR LIGAND SUPERF
TUMOR NECROSIS FORM.
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CONFLICT
SEQUENCE
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EMBL; AB035138; BAA90294.1; -.
EMBL; AB035139; BAA90295.1; -.
EMBL; AB035140; BAA90296.1; -.
HSSP; P01375; 4TSV.
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the European Bioinformatics Institute. There as
use by non-profit institutions as long as i
modified and this statement is not removed. Us
MEDLINE-95127560; PubMed-7826947; Takahashi T., Tanaka M., Inazawa
                                                                                       SEQUENCE FROM N.A.
MEDLINE-95105731;
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Mammalia; Eutheria; Primates;
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                                           lymphocytes.
J. Exp. Med.
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                       SEQUENCE FROM N.A.
                                                                                                                         NCBI_TaxID=9606
                                                                                                                                                          Homo sapiens (Human)
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IPR000478; TNF_family.
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N-LINKED (GLCNAC. . .) (POTENTIAL).

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CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                             Score 50;
Pred. No.
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Tanaka M., Itai T., Adachi M., Nagata S.;
"Downregulation of Fas ligand by shedding.";
Nat. Med. 4:31-36(1998).
-I- FUNCTION: Cytokine that binds to TNFRSF6/FAS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Schneider P., Bodmer J.-L., Holler N., Mattmann C. Terskikh A., Peitsch M.C., Tschopp J.;
"Characterization of Fas (Apo-1, CD95)-Fas ligand
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Zeytun A., Nagarkatti M., Nagarkatti P.S.;
"Isolation and characterization of a new naturally
human Fas ligand that is expressed only in membrane
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PubMed-9427603;
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splenomegaly.
- SIMILARITY: BELONGS TO
- DATABASE: NAME=PROW; I
WWW-"http://www.ncbi.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            SUBUNIT: HOMOTRIMER (PROBABLE).
SUBCELLULAR LOCATION: TYPE II MEMBRANE
INTO THE EXTRACELLULAR FLUID, PROBABLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           runciion: Cytokine that binds to TNFRSF6/FAS, a receptor that transduces the apoptoblic signal into cells. May be involved in cytotoxic T cell mediated apoptosis and in T cell development. TNFRSF6/FAS-mediated apoptosis may have a role in the induction of peripheral tolerance, in the antigen-stimulated suicide of mature T cells, or both. Binding to the decoy receptor TNFRSF6B/DcR3 modulates the affect.
                                                                                                                               lymphoproliferative syndrome (ALPS), syndrome (CSS), a childhood syndrome and thrombocytopenia with massive lym
                                                                                                                                                                                                                                    proteolytic processing.
DISEASE: Defects in TNFSF6 are a
                                                                                                                                                                                                                                                                                             PTM: N-glycosylated. PTM: The soluble form
                                                                                                                                                                                                                                                                                                                                                             are produced by alternative
                                                                                                                                                                                                                                                                                                                                                                                                  SURFACE.
ALTERNATIVE PRODUCTS:
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                                     TO THE TUMOR NECROSIS FY NOTE-PROW 2:59-69(2001)
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lving hemolytic anemia
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RESULT 4
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                                                                                                                                                                                                                                                                                                                                         ProDom; PD002012; TNF_abc; 1.
SMART; SM02207; TNF; 1.
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PROSITE; PS50049; TNF_2; 1.
Cytokine; Apoptosis; Transmembrane; Glycoprotein; Signal-anchor;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      or send an email to license@isb-sib.ch).
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                                                                           SEQUENCE
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                                                                                                                                                                                                       CARBOHYD
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                                                                                              MUTAGEN
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                                                                                                                                                                                                                                                                                                                                                                                                                InterPro;
109
                  1 KELAELRESTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                            L; X89102; CAA61474.1; -.
L; U08137; AAC50071.1; -.
L; U11821; AAC50124.1; -.
L; D38122; BAA07320.1; -.
L; AF288573; AAC60017.1; -.
L; BC017502; AAH17502.1; -.
L; AB013303; BAA32542.1; -.
KELAELRESTS
                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                              IPR003636;
                                                                           281 AA;
                                                                                                                                                                                                                                                                                                                          splicing; Antigen
                                     Conservative
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129
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206
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102
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CLEAVAGE.
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N-LINKED (GLCNAC. ..) (POT
N-LINKED (GLCNAC. ..) (POT
STSQMHTASSL -> ATPVHPLKKRS
                                    Score 50; DB Pred. No. 0.0; Mismatches
                                                                                                      Y->F,R: LOWERS BINDING TO ABOLISHES CYTOTOXITY.
                                                                                                                                  MISSING (IN ISOFORM 2).
P->D,F,R: LOWERS BINDING TO THERSES
AND REDUCES CYTOTOXITY MORE THAN A
                                                                                                                                                                                                                                                      (POTENTIAL).
EXTRACELLULAR
                                                                                                                                                                                                                                                                          SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
                                                                                                                                                                                                                                                                                            TUMOR NECROSIS FACTOR LIGAND MEMBER 6, SOLUBLE FORM.
                                                                                                                                                                                                               POTENT IAL.
                                                                                                                                                                                                                                              PRO-RICH
                                                                                                                                                                                                                                                                                    CYTOPLASMIC
                                                                                                                                                                                                                                                                                                                 MEMBER 6, MEMBRANE FORM.
                                                                                             F->L: ABOLISHES BINDING
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                                                                                                                                                                                                                                                                                                                          TUMOR NECROSIS FACTOR LIGAND
                                                                           A8A6EB358246E9BB
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                                               0.032;
                                                         DB 1;
                                                                                                                                                                                                                                                                                     (POTENTIAL)
                                                                                                                                                                                                                                                      (POTENTIAL).
                                     0
                                                       Length
                                                                           CRC64;
                                     Indels
                                                                                                                                                                                  (POTENTIAL).
(POTENTIAL).
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                                                                                                                TNFRSF6
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KELAELREFTN 116

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CARBOHYD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Suda T., Takahashi T., Golstein P., Nagata S.;
"Molecular cloning and expression of the Fas ligar
of the tumor necrosis factor family.";
Cell 75:1169-1178(1993).
-I- FUNCTION: Cytokine that binds to TNFRSF6/FAS.
                                                                             SEQUENCE
                                                                                                                                                                                                                TRANSMEM
                                                                                                                                                                                                                            DOMAIN
                                                                                                                                                                                                                                                      CHAIN
                                                                                                                                                                                                                                                                                  CHAIN
                                                                                                                                                                                                                                                                                                                                   ProDom; PD002012; TNI SMART; SM00207; TNF;
                                                                                                                                                                                                                                                                                                                                                                       EMBL; U03470; AAC52129.1; -.
HSSP; P01375; 4TSV.
InterPro; IPR003636; TNF_abc.
InterPro; IPR000478; TNF_family.
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                              Pfam; PF00229; TNF;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           <del>:</del>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=10116;
[1]
                                                                                                                                                                                                                                                                                                         PROSITE;
                                                                                                                                                                                                                                                                                                                       PROSIT
 منز
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         transduces the apoptotic signal into cells. May be involved in cytotoxic T cell mediated apoptosis and in T cell development. TNFRSP6/FAS-mediated apoptosis may have a role in the induction of peripheral tolerance, in the antigen-stimulated suicide of mature T cells, or both. Binding to the decoy receptor TNFRSF6B/DCR3 modulates its effects (By similarity).

SUBCELLULAR LOCATION: Type II membrane protein and secreted (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KIDNEY AND LUNG.

INDUCTION: BY PMA/IONOMYCIN AND CONCAVALIN/INTERLEUKIN-2.

PYM: The soluble form derives from the membrane form by proteolytic processing (By similarity).

SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         similarity).
TISSUE SPECIFICITY: EXPRESSED IN ACTIVATED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                THYMOCYTES. MODERATE
 KELAELRESTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   necrosis
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                        Similarity
9; Conserv
                                                                                                                                                                                                                                                      100207; TRE_1; 1.

PS00251; TNE_1; 1.

PS50049; TNE_2; 1.

PS50049; Transmembrane; Glycoprotein; Signal-anchor. |

TUMOR NECROSIS FACTOR LIGAND SUPERFAL

TUMOR NECROSIS FORM.

SUPERFAL
                                                                           100
45
126
199
116
247
278
                          Conservative
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69
58
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257
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                        Score 41; DB Pred. No. 1.5; 1; Mismatches
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                                                                                      N-LINKED
N-LINKED
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CLEAVAGE (BY SIMILARITY).
POTENTIAL.
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SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
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                                                                                                                                                                                       EXTRACELLULAR
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                                                                                                                                                                                                                                                     MEMBER 6, MEMBRANE FORM. TUMOR NECROSIS FACTOR LI
                                                                                                                                                                        PRO-RICH.
                                                                                                                                                                                                  (POTENTIAL)
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Sciurognathi; Muridae;
                                                                          -LINKED (GLCNAC. ..) (POTENTIAL).
-LINKED (GLCNAC. ..) (POTENTIAL).
-LINKED (GLCNAC. ..) (POTENTIAL).
2898E18A862CEAC6 CRC64;
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                          1;
                                              Length 278;
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"Polymorphism activity.";
Proc. Natl. Ac
                                                          Kayagaki N
Yagita H.;
                                                                                                                                                                                                                                                                                                                           STRAIN-C3H; TISSUE-Spleen;
MEDLINE-20021694; PubMed=10552956;
Ayroldi E., D'Adamio F., Zollo O., Agostini M., Moraca R.,
Cannarile L., Migliorati G., Delfino D.V., Riccardi C.;
"Cloning and expression of a short Fas ligand: A new alternatively
spliced product of the mouse Fas ligand gene.";
Blood 94:3456-3467(1999).
                                                                                                                                                                                  CHARACTERIZATION OF VARIANT GLD.
MEDLINE-96091792; PubMed=7495745;
Hahne M., Peitsch M.C., Irmler M.,
Rousseau M., Bron C., Renno T., Fre
"Characterization of the non-function."
Int. Immunol. 7:1381-1386(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         [E].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Peitsch M.J., Tschopp J.J.;
"Comparative molecular modelling
of the TNF family.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             mutation in the Fas ligand.";
Cell 76:969-976(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Suda
                                                                                                                       STRAIN-Various;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. (ISOFORM FASL). MEDLINE-95196085; PubMed-7889405;
                                                                                                      PubMed-9108079;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Fenner M.H., Shioda T.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Lynch D.H., Watson M.L., Alderson M.R., Frough T., Gibson M., Davis-Smith T., Smil Trough T., Guisand gene is mutated in TNF family gene cluster.";

Immunity 1:131-136(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN-C57BI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Generalized lymphoproliferative disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. (ISOFORM FASL).
MEDLINE-94185175; PubMed-7511063;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vert
Mammalia; Eutheria; Rodentia; Sciurognathi;
NCBI_TaxID=10090;
                                                                                                                                               /ARIANTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-95388076;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus (Mouse)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    acids."
  Acad.
                                                                              Yamaguchi N.,
                                       of murine
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (ISOFORM FASL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (ISOFORM
                                                                                                                                                                                                        C., Irmler M., Schroeter M., Lo, Renno T., French L., Tschopp the non-functional Fas ligand
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Fas
                                                                                                                                             GLY-218
U.S.A. 94:3914-3919(1997)
                                       Fas ligand that affects
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Isselbacher K.J
s ligand differs
                                                                              Nagao F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FASLS).
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T., Smith C.A., Hunter K
ated in gld mice and is p
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                                                                                Matsuo
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                                       biological
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                                                                                  Okumura
                                                                                                                                                                                                            mice.";
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the Euro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -i- FUNCTION: Cytokine that binds to TNFRSF6/FAS, a receptor that transduces the apoptotic signal into cells. May be involved in cytotoxic T cell mediated apoptosis and in T cell development. TNFRSF6/FAS-mediated apoptosis may have a role in the induction of peripheral tolerance, in the antigen-stimulated suicide of mature T cells, or both. Binding to the decoy receptor TNFRSF6B/DcR3 modulates its effects (By similarity).
-i- SUBUNIT: HOMOTRIMER (PROBABLE).
-i- SUBCELLULAR LOCATION: Type II membrane protein (isoform FASL);
Secreted (isoforms FASL and FASLS).
Secreted (isoforms FASL and FASLS).
-i- ALTERNATIVE PRODUCTS: 2 ISOFORMS; FASL (SHOWN HERE) AND FASLS; ARE PRODUCED BY ALTERNATIVE SPLICING. ISOFORM FASL MEDIATES APOPTOSIS
WHILE ISOFORM FASLS PREVENTS APOPTOSIS INDUCED BY FAS/FASL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                      SEQUENCE
                                                                                 VARIANT
                                                                                                           VARIANT
                                                                                                                                      VARIANT
                                                                                                                                                                             CARBOHYD
                                                                                                                                                                                           CARBOHYD
                                                                                                                                                                                                         CARBOHYD
                                                                                                                                                                                                                    DISULFID
                                                                                                                                                                                                                                    SITE
                                                                                                                                                                                                                                                                                                 TRANSMEM
                                                                                                                                                                                                                                                                                                                DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF00229; TNF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MGD; MGI:99255;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PTM: The soluble form derives from the membrane form by proteolytic processing (By similarity).

DISEASE: A DEFICIENCY IN THIS PROTEIN IS THE CAUSE OF GENERA LYMPHOPROLIFERATION DISEASE (GLD), AN AUTOSOMAL RECESSIVE DI RESPONSIBLE FOR LYMPHADENOPATHY AND AUTOANTIBODY PRODUCTION. SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             European Bioinformatics Institute. There are no restrictions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; U06948; AAA17800.1; -.
; U10984; AAA19778.1; -.
; S76752; AAB33780.1; -.
;; U58995; AAB02915.1; -.
;; AF119335; AAD52106.1; -.
;; P01375; 4TSV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INTERACTION
                                                                                                                                                                                                                                                                                                                                                                                                                                  PD002012; TNF_abc; 1.
SM00207; TNF; 1.
  Similarity
9; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IPR003636; TNF_abc. IPR000478; TNF_family.
                                                      279
  Conservative
                                                                                                                                                              101
45
127
127
200
117
182
258
                                                                                                                                      184
                                                      ß
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tnfsf6.
                                                                                                                                    279
51
128
231
117
117
182
248
258
210
                                                                                                                                                                                                                                                                                                78
100
                                                                                                          218
                                                      31442
            82.0%;
81.8%;
                                                       ₹.
                                                                                                   POTENTIAL:

N-LINKED (GLCNAC. . .) (POTENTIAL).

MISSING (IN ISOFORM FASLS).

T -> A (IN STRAINS BALB/C AND DBA;

E -> G (IN STRAINS BALB/C AND DBA;
 Score 41; DB Pred. No. 1.5; 1; Mismatches
                                                                                 ENHANCES
E -> G (I
ENHANCES
F -> L (I
                                                                                                                                                                                                                                                                                              TUMOR NECROSIS FACTOR LIGAND SUPERFAMILY
MEMBER 6, SOLUBLE FORM (BY SIMILARITY).
CYTOPLASMIC (POTENYIAL).
SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
                                                                   or
                                                                                                                                                                                                                               CLEAVAGE (BY
                                                                                                                                                                                                                                                                      EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                      (POTENTIAL)
                                                   37972E2728E0A1CA CRC64;
                                                                   (IN GLD; ABOLISHES BINDING RECEPTOR).
                                                                                             CYTOTOXICITY)
                                                                                                                                                            (GLCNAC. .) (POTENTIAL).
(GLCNAC. .) (POTENTIAL).
(GLCNAC. .) (POTENTIAL).
(GLCNAC. .) (POTENTIAL).
             1.5;
                                                                                                                                                                                                                                 SIMILARITY).
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                          1;
 ;
                          Length 279
 Indels
                                                                                                                                                                                                                                                                                                                                                                SUPERFAMILY
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DISEASE
                                                                               엵
 Gaps
                                                                                 FASL
0
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RESULT 6
   SEQUENCE FROM N.A.
STRAIN-Guanxi bama minghaling yang Y.;
Zhu N., Young Y.;
"Molecular cloning and submitted (APR-2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q9BEA8; Q95N10; Q95M04;
15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Tumor necrosis factor ligand superfamily member
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDILINE-21322533; PubMed-11429161; Muneta Y., Shimoji Y., Inumaru S., Mor "Molecular cloning, characterization, 11gand (CD95 ligand).";
                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation—the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sus scrofa (Pig).
Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tsuyuki S., Kono M., Bloom E.T.;
"Cloning and potential utility of porcine Fas in porcine cells protects them from attack by Submitted (JUL-2001) to the EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. TISSUE-Lymphoid; Tsuyuki S., Kono M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted [3]
                                                                                                                                                                                                                      ÷
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. MEDLINE-21322533;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TNFSF6 OR FASL.
                                                                                                                                                                                                                                                                                                                                                                                                      with human gene.
                                                                                                                                                                                                                                                                                                                                                                                                           "Porcine Fas-ligand gene:
                                                                                                                                                                                                                                                                                                                                                                                                                                   Motegi-Ishiyama Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                   PubMed=11792426;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN-Landrace
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=9823;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   igand)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         107
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Interferon
                                                                                                                                                                                                                                              . Immunol. 38:581-586(2002).

FUNCTION: Cytokine that binds to TNFRSF6/FAS, a receptor that transduces the apoptosit signal into cells. May be involved in cytotoxic T cell mediated apoptosis and in T cell development. TNFRSF6/FAS-mediated apoptosis may have a role in the induction of peripheral tolerance, in the antigen-stimulated suicide of mature T cells, or both. Binding to the decoy receptor TNFRSF6B/DcR3 modulates its effects (By similarity).

SUBQUIT: Homotrimer (Probable).

SUBQUITAR LOCATION: Type II membrane protein and secreted (By SUBCELLIJLAR LOCATION: Type II membrane protein.
                                                                                                                                                                      proteolytic processing SIMILARITY: BELONGS TO
                                                                                                                                                                                                   PIM: The soluble form derives
                                                                                                                                                                                                                      INDUCTION: By IL-18.
                                                                                                                                                                                                                                   similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KELAELRESTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KELAELREFTN
 AB027297;
AY033634;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cytokine Res.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD; Q95M04;
BAB40919.1;
AAK56449.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 x Large
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         117
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   miniature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Chordata; Craniata; Vertebrata;
Cetartiodactyla; Suina; Suidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                   Nakajima Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ç
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      characterizaion of porcine Fas ligand cDNA.";
o the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Yorkshire white;
                                                                                                                                                                                                                                                                                                                                                                                                                    genomic
                                                                                                                                                                 derives from the membrane torm by (By similarity).
THE TUMOR NECROSIS FACTOR FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21:305-312(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   pig;
                                                                                                                                                                                                                                                                                                                                                                                                                                   Hoka S.,
                                                                                                                                                                                                                                                                                                                                                                                                                    sequence analysis and comparison
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mor1 Y.;
on, and expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE-Thymocytes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ð
                                                                                                                                                                                                                                                                                                                                                                                                                                    Takagaki Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ligand: overexpression human cytolytic cells."; databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   σ
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Sus.
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EMBL; EMBL; HSSP;

AF397407; AAK84408.1; AB069764; BAB64291.1;

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В
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                                                                                                                                                                                                                                                                                                                         SUC1_ARCFU
SUC1_ARCFU
STANDARD;
PRT; 38:
C 028732;
C 028732;
T 30-MAY-2000 (Rel. 39, Created)
T 15-JUN-2002 (Rel. 41, Last sequence updated)
T 15-JUN-2002 (Rel. 41, Last annotation updated)
Succinyl-CoA synthetase beta chain 1 (EC November 1)
Succinyl-CoA synthetase beta chain 1 (EC November 2)
Succinyl-CoA synthetase beta chain 1 (EC November 2)
Succinyl-CoA synthetase beta chain 1 (EC November 2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local
                                                              Klenk H.-P., Clayton R.A., Tomb J.-F., White O., Nelson K.E., Ketchum K.A., Dodson R.J., Gwinn M., Hickey E.K., Peterson J.D., Richardson D.L., Kerlavage A.R., Graham D.E., Kyrpides N.C., Fileischmann R.D., Quackenbush J., Lee N.H., Sutton G.G., Gill S., Kirkness E.F., Dougherty B.A., McKenney K., Adams M.D., Loftus B., Peterson S., Reich C.I., McNeil L.K., Badger J.H., Glodek A., Zhou Overbeek R., Gocayne J.D., Weldman J.F., McDonald L., Utterback T., Cotton M.D., Spriggs T., Artiach P., Kaine B.P., Sykes S.M., Sadow P.W., D'Andrea K.P., Bowman C., Fujil C., Garland S.A., Mason T.M., Olsen G.J., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DISULFID CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DOMAIN
DOMAIN
            "The complete genome sequence of reducing archaeon Archaeoglobus Nature 390:364-370(1997).
-I- CATALYTIC ACTIVITY: ATP + su
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SMART; SM00207; INE,

PROSITE; PS00251; TNF_1; 1.

PROSITE; PS50049; TNF_2; 1.

PROSITE; PS50049; TNF_2; 1.

TUMOR NECROSIS FACTOR LIGAND SUPERFAMILY

TUMOR NECROSIS FACTOR FORM.

SUPERFAMILY

TOWNS SUPERFAMILY
                                                                                                                                                                                                                                  STRAIN-VC-16 / DSN
                                                                                                                                                                                                                                                                                   Archaeoglobus fulgidus.
Archaee; Euryarchaeota; Archaeoglobi;
Archaeoglobaceae; Archaeoglobus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRINTS; PR01234; TNECROSISFCT.
PRODOZ012; TNF_abc; 1.
SMART; SM00207; TNF; 1.
PROSITE; PS00251; TNF_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR003636; TNF_abc.
InterPro; IPR000478; TNF_family.
Pfam; PF00229; TNF; 1.
                                                                                                                                                                                                                  STRAIN-VC-16 / DSM 4304 / ATCC 49558; MEDLINE-98049343; PubMed-9389475;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 KELAELRESTS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KELTELRESAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9; Conserv
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282
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45
130
203
185
251
261
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   282
70
56
131
234
251
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103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      31756 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               82.0%;
81.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
F -> L (IN REF 4).
T -> P (IN REF 2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               score
Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEMBER 6, SOLUBLE FORM (BY SIMILARITY).
CYTOPLASMIC (POTENTIAL).
SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEMBER 6, MEMBRANE FORM.
TUMOR NECROSIS FACTOR LIGAND SUPERFAMILY
MEMBER 6, SOLUBLE FORM (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLEAVAGE (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRO-RICH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EXTRACELLULAR (POTENTIAL).
                                    of the hyperthermophilic, is fulgidus.";
              succinate +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -> L (IN REF. 4).
-> P (IN REF. 2).
6743DAA1145671FB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                      lon update)
1 (EC 6.2.1.5) (SCS-beta 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           41;
                                                                                                                                                                                                                                                                                                                                                                  update)
                                                                                                                                                                                                                                                                                                                                                                                                          382 AA
                                                                                                                                                                                                                                                                                                 Archaeoglobales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 1;
              8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 282
              ADP
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              +
                                                  sulphate:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0,
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                                                                                                                                   Zhou L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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RESULT 8
VIEN_NPVAC
ID VIEN_N
AC P24647
OT 01-MAR
DT 01-NOV
DT 01-
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Best Local S
Matches 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PIGH, FIGURE TIGRO1016; SUCCOADETA; I.
TIGRFAN'S; TIGRO1217; SUCCINYL_COA_LIG_3; 1.
PROSITE; PS01217; SUCCINYL_COA_LIG_3; 1.
Ligase; Tricarboxylic acid cycle; Complete proteome.
Ligase; Tricarboxylic acid cycle; Complete proteome.
An An 42204 MW; 418ACBA41E64DA9F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Carson D.D., Summers M.D., Guarino L.A., "Molecular analysis of a baculovirus reg Virology 182:279-286(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for commodified and this statement is not removed. Usage by and for commodified and this statement is not removed.
                                                                                                 VIFOLOGY 202:586-605(1994).

11- FUNCTION: IE-N AUTOREGULATES ITS OWN EXPRESSION AND STIMULATES BOTH IE-1 AND IE-0 IN TRANSIENT ASSAYS. THE STIMULATION OF IE-: EXPRESSION MAY ACCOUNT FOR THE AUGMENTING ACTIVITY OF IE-N IN IE-1 MEDIATED TRANS-ACTIVATION OF THE 39K PROMOTER.

11- SIMILARITY: TO OPMUND IMMEDIATE-EARLY PROTEIN IE-2.

-1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
                                                                                                                                                                                                                                                                                 "The complete DNA sequence polyhedrosis virus.";
                                                                                                                                                                                                                                                                                                           Ayres M.D.,
"The comple
                                                                                                                                                                                                                                                                                                                                MEDLINE-94303173; PubMed-8030224; Ayres M.D., Howard S.C., Kuzio J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Viruses; dsDNA viruses, Nucleopolyhedrovirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-MAR-1992 (Rel. 21, Created)
01-NOV-1995 (Rel. 32, Last squence update)
16-CCT-2001 (Rel. 40, Last annotation update)
Immediate-early regulatory protein IE-N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VIEN_NPVAC P24647;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF00549; ligase-CoA; Pfam; PF02222; ATP-grasp; ]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HSSP; P07460;
TIGR; AF1540;
                            between
                                                                                                                                                                                                                                                                                                                                                                                       STRAIN-C6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR003135; ATP-grasp.
InterPro; IPR000303; CoA_ligase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=91220660; PubMed=2024466;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID-46015;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Autographa californica nuclear
                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 ELAELREST
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                                            SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ELAELREAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AE000996; AAB89706.1; ALT_INIT.
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8; Conser
                            the
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  Swiss Institute
Bioinformatics 1
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                                                                                                                                                                                                                                                                                                           of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      lear polyhedrosis virus (ACMNPV).
RNA stage; Baculoviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 38;
Pred. No.
                            of Bioinformatics
                                                                                                                                                                                                                                                                                                         Autographa californica
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      regulatory gene.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 1;
7.7;
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(See http://www.isb-sib.ch/announce/

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Best Local S
Matches 8
                                                                                                                                                                                                                                                                                                            STRAIN-JA.1 / DSM 2661 / ATCC 43067;

STRAIN-JA.1 / DSM 2661 / ATCC 43067;

Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,

Bult C.J., White O., Olsen G.J., Zhou L., Clayton R.A., Gocayne J.D.,

Sutton G.G., Blake J.A., FitzGerald L.M., Clayton R.A., Gocayne J.D.,

Kerlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,

Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,

Scott J.L., Geoghagen N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D.,

Utterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,

Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,

Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.,

"Complete genome sequence of the methanogenic archaeon, Methanococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZN_FING
CONFLICT
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DOMAIN
DOMAIN
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PROSITE; PS50089; ZF_RING_2; 1.
Early protein; Transcription regulation; Trans-acting Activator; Repeat; Zinc-finger; DNA-binding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            D58844;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
16-OCT-2001 (Rel. 40, Last annotation update)
16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL;
                                                                                                                                  Zerler B., Myers P.A., Escalante H., Roberts R.J.;
Unpublished observations (XXX-1997).
-!- FUNCTION: RECOGNIZES THE DOUBLE-STRANDED SEQUENCE GGNCC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Archaea; Euryarchaeota; Methanococci; Methanococcales; Methanocaldococcaceae; Methanocaldococcus.
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                    "Complete genome sequence jannaschii.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Methanococcus jannaschii.
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                                                                                                                                                                                                                    CHARACTERIZATION.
                                                                                                                                                                                                                                                                        Science 273:1058-1073(1996).
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                                                                                                           CATALYTIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                            C ACTIVITY: Endonucleolytic cleavage of DNA to give double-stranded fragments with terminal 5'-phosphates.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAA66781.1; -.
                                                                                                           ACTIVITY: Endonucleolytic
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POLY-GLN.
GLU-RICH (ACIDIC).
RING-TYPE.
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Pred. No.
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X 4 AA TANDEM REPEATS
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InterPro; IPR003593; ANA_ATPase.
InterPro; IPR003439; ABC_transportr.
Pfam; PF000005; ABC_tran; 2.
ProDom; PD000006; ABC_transportr; 2.
SMART; SM00382; AAA; 1.
PROSITE; PS00211; ABC_TRANSPORTER; 1.
Hypothetical protein; ATP-binding; Transporter; 1.

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33 412 445 494 519 554 662

POTENTIAL.
POTENTIAL.
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POTENTIAL. POTENTIAL. POTENTIAL

ransport

ATP-binding; Transmembrane; Glycoprotein;

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RESULT 10
YN99_YEAST
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Query Match
Best Local 9
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01-OCT-1996 (Rel. 34, Created)

01-OCT-1996 (Rel. 34, Last sequence update)

15-JUL-1999 (Rel. 38, Last annotation update)

Probable ATP-dependent transporter YNR070W.

YNR070W OR N3568.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation—the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE OF 1-1054 FROM N.A.

Duesterhoeft A., Floeth M., Fritz C., Heuss-Neitzel D.,

Hilbert H., Moestl D.;

Hilbert H., Moestl D.;

Submitted (MAY-1996) to the EMBL/GenBank/DDBJ databases.

-!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).

-!- SIMILARITY: BELONGS TO THE ABC TRANSPORTER FAMILY. PDR5 SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; U67585; AAB99461.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. Andre B., Iraqui H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hydrolase; Endonuclease; Nuclease; Restriction system;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TIGR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REBASE;
                                                                                                                                                                                                                                     EMBL; Z71685; CAA96352.1; -. EMBL; Z71686; CAA96354.1; -. SGD; S0005353; YNR070W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Andre B., Iraqui Houssaini I., Urrestarazu L.A., Vissers Submitted (MAY-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; Saccharomycetaceae; Saccharomyces.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Saccharomyces cerevisiae (Baker's yeast).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  126 KENKELREATS 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 KELAELRESTS
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8; Conserv
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370 AA;
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Pred. No.
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RP SEQUENCE FROM N.A.

RY MEDLINE-21638749; PubMed-11780052;

RA Deloukas P., Matthews L.H., Ashurst J., Burton J., Gilbert J.G.R.,

RA Deloukas P., Matthews L.H., Ashurst J., Babbage A.K., Bagguley C.L.,

RA Deloukas P., Matthews L.H., Bates K.N., Beard L.M., Beare D.M.,

RA Bailey J., Barlow K.F., Bates K.N., Beard L.M., Beare D.M.,

RA Beasley O.P., Bird C.P., Blakey S.E., Bridgeman A.M., Brown A.J.,

RA Beasley J., Barlow K.F., Bates K.N., Carder C., Carter N.P.,

RA Buck D., Burrill W.D., Butler A.P., Carder C., Carter N.P.,

RA Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.Y., Clee C.M.,

RA Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.Y., Clee C.M.,

RA Coulson A., Coville G.J., Deadman R., Dhami P.D., Dunn M.,

RA Coulson A., Coville G.J., Deadman R., Dhami P.D., Dunn M.,

RA Caffham D.V., Griffiths C., Griffiths M.N.D., Gwilliam R., Hall R.E.,

RA Grafham D.V., Griffiths C., Griffiths M.N.D., Gwilliam R., Hall R.E.,

RA Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J.,

RA Huckle E., Hunt A.R., King A., Knights A., Lalrd G.K., Lawlor S.,

RA Kay M.P., Kimberley A.M., King A., Knights A., Lalrd G.K., Lawlor S.,

RA Kay M.P., Kimberley A.M., King A., Knights A., Lalrd G.K., Lawlor S.,

RA Marsh V.L., Martin S.L., McConnachie L.J., McLay K., McMurray A.A.,

RA Milne S.A., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.,

RA Oliver K., Parker A., Patel R., Pearce T.A.V., Peck A.I.,

RA Nice C.M., Ross M.T., Scott C.E., Sehra H.K., Shownkeen R., Sims S.,

RA Swann R.M., Sycamore N., Taylor R., Tee L., Thomas D.W., Thorpe A.,
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Nomura N., Ohara O.;
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Mammalia; Eutheria;
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A0552.
no Bapiens (Human),
no Bapiens (Human),
Netazoa; Chordata; C
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(Rel. 38, Last sequence up
(Rel. 41, Last annotation
1 protein KIAA0552.
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1e+02;
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RESULT 12

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AC 01076
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DT 16-00
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DT 116-00
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SYI_MYCTU STANDARM;
Q10765; O06181;
01-OCT-1996 (Rel. 34, Created)
01-CCT-1996 (Rel. 34, Last sequence upd.
16-OCT-2001 (Rel. 40, Last annotation u
                                                                                                                                                                                                                                                 MEDLINE-98295987; PubMed-9634230; Garnier T., Churcher C., Harris Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Badcock K., Besham D., Brown D., Chillingworth T., Connor R., Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L., Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J., Rutter S., Seeger K., Skelton S., Squares S., Squares R., Sulston J.E., Taylor K., Whitehead S., Barrell B.G.; "Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence.";
SEQUENCE FROM N.A.

STRAIR-CDC 1551 / Oshkosh:
Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
Fleischmann R.D., Dodson R., Gwinn M.L., Haft D., Hickey E.,
Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg
Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula
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EMBL; AL121891; CAC09910.1; -.
Hypothetical protein; Colled co
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID-1773;
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Bentley
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D.R., Bec
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Beck
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RESULT 13
YOBO_BACSU
ID YOBO_B
AC P45931
DT 01-NOV
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DE HYPOTH
GN YOBO.
OS Bactl1
OC Bacter
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RN [1]
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RR SEQUEN
RX MEDLIN
RA TAKEMA
RT TEARTA
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Best Local S
Matches
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01-NOV-1995
15-JUN-2002
STRAIN-168 / JH642;

MEDLINE-97124195; PubMed-8969508;

Mizuno M., Masuda S., Takemaru K.

Kobayashi Y.;

*Systematic sequencing of the 283
                                                                                                                                                                                        STRAIN=168 / JH642;
MEDLINE=95219086; PubMed=7704261;
MEDLINE=95219086; PubMed=7704261;
Makemaru K.-I., Mizuno M., Sato T., Takeuchi M., Kobayashi Takemaru K.-I., Mizuno M., Sato T., Takeuchi M., Kobayashi Tokemaru K.-I., Mizuno M., Sato T., Takeuchi M., Kobayashi Medili M., Mizuno Mizuno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tuberculist; Rv1536; -...
InterPro; IPR002300; tRNA-synt_la.
InterPro; IPR001412; tRNA-synt_li.
InterPro; IPR002301; tRNA-synt_li.e.
pfam; PF0013; tRNA-synt_l; 1.
PRINTS; PR00984; TRNA-SYNTHILE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HSSP;
TIGR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases
-!- CATALYTIC ACTIVITY: ATP + L-isoleucine + tRNA(Ile)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE; PS00178; AA_TRNA_LIGASE_I; 1.
Aminoacyl-trNa synthetase; Protein bisynthesis;
Metal-binding; Zinc; Complete proteome.

SITE 53 63 "HIGH" REGION.

SITE 619 623 "KMSKS" REGION.

BINDING 622 622 ATP (BY SIMILARITY).

SEQUENCE 1041 AA; 117339 MW; B5023822848E08C6
                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacillus subtilis.
Bacteria; Firmicutes;
                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 P45931;
                                                                                                                                           SEQUENCE FROM N.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              972
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diphosphate + L-isoleucyl-trnA(Ile).
cofactor: BINDS 1 ZINC ION (BY SIMILARITY).
SUBCELLULAR LOCATION: Cytoplasmic.
SIMILARITY: BELONGS TO CLASS-I AMINOACYL-TRNA SYNTHETASE FAMILY.
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MT1587; -.
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AE007025; AAK45854.
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7; Conser
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(Rel. 32, Last sequence update)
(Rel. 41, Last annotation update)
1 protein yqbO.
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"HIGH: REGION.
3 "KMSKS" REGION.
23 "KMSKS" REGION.
22 ATP (BY SIMILARITY).
117339 MW; B5023822848E08C6 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacillales; Bacillaceae;
        of the 283 kb 210 degrees-232 degrees region
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Pred. No.
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                                                       K.-I., Hosono S.,
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                                                          Sato T., Takeuchi M.,
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                                                                                                                                   Matches
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EMBL; D84432; BAA12411.1; -.
EMBL; Z99117; CAB14544.1; -.
Subtitist; BG11286; yqbo.
InterPro; IPR000189; SLT_domain.
Pfam; PF01464; SLT; 1.
Hypothetical protein; Complete pr
SEQUENCE 1585 AA; 171030 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             the Bacillus subtilis genome containing the skin element and many sporulation genes."; Microbiology 142:3103-3111(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gene 165:GC37-GC51(1995).
-!- SIMILARITY: STRONG, TO B.SUBTILIS XKDO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=96084975; PubMed=7489895;
Medigue C., Moszer I., Viari A., Danchin A.;
"Analysis of a Bacillus subtilis genome fragment using a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-98044033; PubMed-9384377; Kunst F., Ogasawara N., Moszer I.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  computer system prototype.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IDENTIFICATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nature 390:249-256(1997).
253 KALAELTESSS 263
                                                                                                                                                                        Loca<sub>1</sub>
                                                              1 KELAELRESTS
                                                                                                                                   Similarity
8; Conser
                                                                                                                                   Conservative
                                                                                                                                                                    Score 34; Pred. No.
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                                                                                                                            1.9e+02;
2;
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P56859;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             between
the Europ
                                                                                                adenovirus type 3.";
Gene 13:387-394(1981).
-I- FUNCTION: THIS PROTEIN IS A STRUCTURAL COMPONENT OF THE VIRION.
MAY HAVE AN ADDITIONAL ROLE DURING ADENOVIRUS MULTIPLICATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SPECIES-Human adenovirus type 7; STRAIN-Gomen; MEDLINS-81261948; PubMed-6266923; MEDLINS-81751948; PubMed-626923; D1jkema R., Maat J., Dekker B.M.M., van Ormondt H., Boyer H.W.; "The gene for polypeptide IX of human adenovirus type 7."; Gene 13:375-385(1981).
                                                                                                                                                                                                                                                                                                                                                                            PIR; A03854; SXAD97.
PIR; B03854; SXAD93.
                                                                                                                                                                                                                                                                                                                                                                                                                                           use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.

SPECIES-Human adenovirus type 3;

MEDLINE-81261949; PubMed-7262560;
 MEDLINE-95287864;
                                                 Eurotiales; Trichocomaceae;
                                                                          Emericella nidulans
                                                                                                                                                                                                     EMENI
                                                                                                                                                                                                                                                                                                                                                     Hexon-associated protein. SEQUENCE 138 AA; 14107
                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; X03000; CAA26764.1; -. EMBL; J01962; AAA42510.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Engler J.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM
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Hexon-associated protein
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| 119 KQVAQLREQT 128
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Ascomycota; Pezizomycotina;
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-I- FUNCTION: THE NADP DEPENDENT REDUCTION OF PAPS INTO SULFITE
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Interpro; IPR004511; cysH.
Pfam; pr01507; PAPS_reduct; 1.
Pfam; pr01507; PAPS_reduct; 1.
TIGR70434; cysH; 1.
Methionine biosynthesis; Cysteine biosynthesis;
SEQUENCE 293 AA; 33978 MW; FCBB379183F21D5F
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SIMILARITY: BELONGS TO THE PAPS REDUCTASE FAMILY. CYSH SUBFAMILY.
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A;Molecule type: mRNA
A;Residues: 1-281 <SCH>
A;Cross references: EMBL:X89102; NID:g887455; PID:g887456
A;Cross references: EMBL:X89102; NID:g887455; PID:g887456
A;Closs references: EMBL:X89102; NID:g887455; PID:g887456
A;Alderson, M.R.; Tough, T.W.; Davis-Smith, T.; Braddy, S.; Falk, B.; Schooley, K.A.;
J. Exp. Med. 181, 71-77, 1995
A;Title: Fas ligand mediates activation-induced cell death in human T lymphocytes.
A;Reference number: I38554; MUID:95105731; PMID:7528780
A;Accession: I38554
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A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 1-281 <RES>
A;Cross references: EMBL:U11821; NID:g595430; PIDN:AAC50124.1; PID:g595431
A;Cross references: EMBL:U11821; NID:g595430; PIDN:AAC50124.1; PID:g595431
B;Mita, E.; Hayashi, N.; Iio, S.; Takehara, T.; Hijioka, T.; Kasahara, A.; Fusamv
Blochem. Biophys. Res. Commun. 204, 468-474, 1994
A;Title: Role of Fas ligand in apoptosis induced by hepatitis C virus infection.
A;Reference number: JC2340; MUID:95071350; PMID:7980502
A;Accession: JC2340; MUID:95071350; PMID:7980502
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138707
Fas ligand - human
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: 49-May-1998 #sequence_revision 29-May-1998 #text_change 21-Jul-2000
C;Accession: 138707; JC2340; S57565; I38554
R;Takahashi, T.: Tanaka, M.; Inazawa, J.; Abe, T.; Suda, T.; Nagata, S.
Int. Immunol. 6, 1567-1574, 1994
A;Title: Human Fas ligand: gene structure, chromosomal location and species specifici A;Reference number: I38707; MUID:95127560; pMID:7826947
A;Accession: I38707
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                                                                                                                                   A;Introns: 151/1; 116/3
C;Keywords: glycoprotein; transmembrane protein
F;80-102/Domain: transmembrane *status predicted <TMM>
F;76,184,250,260/Binding site: carbohydrate (Asn) (covalent) *status
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A;Gene: FasL
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A; Residues: 1-281 <RE2>
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A; Status: preliminary
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A; Residues: 1-281 <MIT>
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1 KELAELRESTS 11

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C:Species: Mus musculus (house mouse)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 05-Nov-1999
C:Accession: A53062
R:Takahashi, T.: Tanaka, M.: Brannan, C.I.: Jenkins, N.A.: Copeland, N.G.: (cell 76, 969-976, 1994
A:Title: Generalized lymphoproliferative disease in mice, caused by a point A:Reference number: A53062; MUID:94185175; PMID:7511063
A:Accession: A53062; MUID:94185175; PMID:7511063
                                                       C;ACCession: C69442
R;Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Fleischmann, R.D.; Querbeek, J.D.; Lee, N.H.; Sutton, G.G.; Glodek, A.; Zhou, L.; Overbeek, R.; Goayne, J.D.; Weidman, J.F. Nature 390, 364-370, 1997
A;Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P. Smith, H.O.; Woese, C.R.; Venton, M.D.; Spriggs, T.; Artiach, P. A;Title: The complete genome sequence of the hyperthermophilic, A;Reference number: A69250; MUID:98049343; PMID:9389475
A;Accession: C69442
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C69442
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C:Species: Rattus norvegicus (Norway rat)
C:Date: 13-Jan-1995 #sequence_revision 13
C:Accession: A49266
                                                                                                                                                                                                                                                                     succinyl-CoA synthetase, beta subunit (sucC-1) homolog - Archaeoglobus fulg
C;Species: Archaeoglobus fulgidus
C;Data: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 16-Jul-1999
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A;Residues: 1-279 <TAK>
A;Cross-references: GB:U0694B; NID:g473564; PIDN:AAA17800.1; PID:g473565
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A;Title: Molecular cloning and expression of the Fas ligand, A;Reference number: A49266; MUID:94084792; PMID:7505205
A;Accession: A49266
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A; Residues: 1-278 <SUD>
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                   type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity 81.0
9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  82.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 41; DB Pred. No. 3; 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 41;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13-Jan-1995 #text_change 05-Nov-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                 Archaeoglobus fulgidus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          caused by a point mutation
                                                                                                                                                                                     K.E.; Ketchum, K.A.; D
G.; Gill, S.; Kirkness,
J.F.; McDonald, L.
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                                                                                                                                           B.P.; Sykes,
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                                                                                                                                                                                                                                  K.A.; Dodsor
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A;Cross-references: GB:AE000996; GB:AE000782; NID:g2689319; PIDN:AAB89706.1; C;Superfamily: succinate-CoA ligase (ADP-forming) beta chain
 Matches
                       Query Match
Local Similarity hes 8; Conser
Conservative
           76.0%;
           Score 38;
Pred. No.
 Mismatches
          DB
16;
                        2
 0
                       Length 383;
 Indels
0
 Gaps
0;
                                                           PID: 9264
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밁 RESULT 220 ELAELREAT 228 ş

2 ELAELREST 10

A;Cross-references: GB:M59422; NID:g332437; PIDN:AAA46701.1; PID:g332438 C;Superfamily: AcMNPV immediate-early protein IE-N C;Keyvords: DNA binding; early protein; tandem repeat; transcription regulation F;34-49/Region: 7-residue repeats F;51-58/Region: 4-residue repeats F;190-196/Region: glutamine-rich Virology 182, 279-286, 1991 A;Title: Molecular analysis A;Reference number: A39150; immediate-early protein IE-N - Autographa californica nuclear polyhedrosis virus
C;Species: Autographa californica nuclear polyhedrosis virus, AcMNPV
C;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 16-Jul-1999 A; Molecule type: DNA A; Residues: 1-408 < CAR> A; Accession: A39150 R; Carson, D.D.; C; Accession: A39150 MIVIMW Matches Query Match Best Local 311 KELSELRAKTS 321 1 KELAELRESTS 11 Similarity 72.7 8; Conservative Summers, M.D.; Guarino, L.A. 74.08; 72.78; of a baculovirus regulatory MUID:91220660; PMID:2024466 Score 37; Pred. No. Mismatches рв 27; 1; <u>ب</u> Length 408, Indels 0 Gaps 0;

밁 8

R;Ayres, M.D.; Howard, S.C.; Kuzio, J.; Lopez-Ferber, M.; Possee, R.D. Virology 202, 586-605, 1994
A;Title: The complete DNA sequence of Autographa californica nuclear pa;Reference number: A72850; MUID:94303173; PMID:8030224
A;Accession: A72869 A; Molecule type: DNA A; Residues: 1-408 < AYR> A; Note: dsDNA virus C;Date: 12-Nov-1999 #sequence_revision 12-Nov-1999 #text_change 11-Jan-2000 early gene transactivator - Autographa californica nuclear polyhedrosis virus C;Species: Autographa californica nuclear polyhedrosis virus, ACMNPV C; Genetics: A;Cross-references: GB:L22858; NID:g510708; PIDN:AAA66781.1; A;Status: C; Accession: A72869 preliminary PID:9559220 nuclear polyhedrosis

Vir

A;Gene: Ac-IE-2 C:Superfamily: ACMNPV immediate-early protein IE-N Š Query Match Best Local Matches 1 KELAELRESTS 11 Ac-IE-2 Similarity 8; Conserv Conservative 74.0%; Score 37; DB Pred. No. 27; 1; Mismatches DB 27; 2 Length 408 Indels 0 Gaps

0

무 311 KELSELRAKTS 321

RESULT 7 A59292 probable type Ξ myosin heavy chain slime mold (Physarum polycephalum) (fragment)

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4

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C;Species: Physarum polycephalum
C;Date: 09-Jun-2000 *sequence_revision 09-Jun-2000 *tex
C;Accession: A59292
R;Bailey, J.; Cook, L.J.; Kilme.Barber, R.; Swanston, F
submitted to GenBank, March 1999
A;Description: Identification of three genes expressed
A;Reference number: A59292
A;Accession: A59292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         hypothetical protein MJ1449 - Methanococcus jannaschii C;Species: Methanococcus jannaschii C;Species: Methanococcus jannaschii C;Date: 13-Sep-1996 *sequence_revision 13-Sep-1996 *text_change 21-Jul-2000 C;Accession: H64480 R;Bult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blab; Reich, C.I.; Overbeek, R.; Kirkness, E.F.; Weinstock, K.G.; Merrick, J.M.; Glodek, rson, J.D.; Sadow, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M.A. Science 273, 1058-1073, 1996 M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M.A. A;Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese A;Title: Complete genome sequence of the methanogenic archaeon, Methanococcus jannasca, Reference number: A64300; MUID:96337999; pMID:8688087
                                                                                                                                                                                                    probable carboxyl-terminal proteinase PA5134 [imported] - Pseudomonas aeruginosa C;Species: Pseudomonas aeruginosa C;Date: 15-Sep-2000 *sequence_revision 15-Sep-2000 *text_change 31-Dec-2000 C;Date: 15-Sep-2000 *sequence_revision 15-Sep-2000 *text_change 31-Dec-2000 C;Accession: B83005 R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, Madman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Gene: mynD
C;Superfamily: kinetoplast-associated protein
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A;Residues: 1-317 <BAI>
A;Cross-references: GB:AJ133501; NID:g4494062; PIDN:CAB39170.1; PID:g4494063
A;Experimental source: strain CU; dev stage plasmodium formation; clone lib
C;Genetics:
                       A; Residues: 1-436 <STO>
                                                                                         A;Title: Complete genome se
A;Reference number: A82950;
A;Accession: B83005
                                                                                                                                                              .; Lory, S.; Olson, M.V. Nature 406, 959-964, 2000
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A; Residues: 1-370 < BUL>
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                                                                    A; Status: preliminary
A;Cross-references: GB:AE004926; GB:AE004091; NID:g9951424; PIDN:AAG08519.1; GSPDB:GN001
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                                                                                                                                                                                                                                                                                                                                                                                                                                         136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11
                                                                                                                   sequence of Pseudomonas aeruginosa PAO1, 50; MUID:20437337; PMID:10984043
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     70.0%;
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ch 1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 35;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2;
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K.; Lim,
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C; Genetics:
A; Gene: PA5134
C; Superfamily: c
                                                                                                                                 submitted to the Protein Sequence Database, A, Reference number: S62944
A; Reference number: S62944
A; Accession: S63402
A; Molecule type: DNA
A; Residues: 1-1053 < DUE>
A; Residues: L-1053 < DUE>
A; Cross-references: EMBL: Z71685; MIPS:YNR070w
A; Experimental source: strain S288C
A;Map position: 14R
C;Superfamily: unassigned ATP-binding cassette proteins; ATP-binding C;Superfamily: unassigned ATP-binding; P-loop; transmembrane protein C;Keywords: ATP, nucleotide binding; P-loop; transmembrane protein F;46-257/Domain: ATP-binding cassette homology <ABCl>
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                                                                      A;Cross-references: SGD:S0005353
A;Map position: 14R
                                                                                                                   C;Genetics:
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A; Residues: 1-625 <COL>
A; Cross-references: GB: AE001240; GB: AE000520;
A; Experimental source: strain Nichols
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Pred. No. 1e+02;
4; Mismatches
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A;Molecule type: DNA
A;Residues: 1-1333 <AND>
A;Residues: 1-1333 <AND>
A;Cross-references: EMBL:Z71685; NID:g1302603; PIDN:CAA96352.1; PID:e239601; PID:g130
A;Experimental source: strain $288C
A;Experiment
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R;Andre, B.; Iraqui Houssaini, I.; Urrestarazu, L.A.;
submitted to the Protein Sequence Database, April 1996
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NALternate names: hypothetical protein N3568
C;Species: Saccharomyces cerevisiae
C;Date: 27-Apr_1996 #sequence_revision 03-May-1996 #text_change 19-Apr-2002
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A;Gene: PH0907
C;Superfamily:
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C71080
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C790thetical protein PH0907 - Pyrococcus horikoshii
C:Species: Pyrococcus horikoshii
C:Species: Pyrococcus horikoshii
C:Date: 14-Aug-1998 *sequence_revision 14-Aug-1998 *text_change 20-Jun-2000
C:Accession: C71080
C:Accession: C71080
R:Kawarabayasi, Y: Sawada, M.: Horikawa, H.; Haikawa, Y.: Hino, Y.: Yamamoi
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                                                                                                                                                                                 A; Experimental source: strain OT3 A; Note: this accession replaces an
                                                                                                                                                                                                                       A;Status: preliminary; nucleic acid sequence not shown; translat
A;Molecule type: DNA
A;Residues: 1-159 <KRAN
A;Cross-references: GB:AP000004; NID:g3236131; PIDN:BAA30001.1;
                                                                                                                                                                                                                                                                                                         A;Title: Complete sequence and gene organization of the genome of a hyper-thermophilic A;Reference number: A71000; MUID:98344137; PMID:9679194 A;Accession: C71080
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A; Residues: 1-74 <STO>
A; Cross-references: GB
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C;Species: Halobacterium sp. NRC-1
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
C;Accession: H84255
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7; Conserv
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8; Conserv
                                                                                                                      hypothetical protein MJECS03
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Pred. No. 2.3e+02;
l; Mismatches 2;
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Hough, D.W.; Maddocks,
                                        Indels
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ks, D.G.; Jab
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Search completed: March 13, Job time: 13.8 secs

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synemin - chicken (fragment)
C;Species; Gallus gallus (chicken)
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 03-Nov-2000
C;Accession: I50721
R;Becker, B.; Bellin, R.M.; Sernett, S.W.; Huiatt, T.W.; Robson, R.M.
Blochem. Blophys. Res. Commun. 213, 796-802, 1995
A;Title: Synemin contains the rod domain of intermediate filaments.
A;Reference number: I50721; MUID:95382823; PMID:7654240
A;Accession: I50721
A;Status: preliminary; translated from GB/EMBL/DDBJ
A:Mologule type. mBNA
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A:Mologule type. mBNA
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A;Map position: 2
A;Introns: 33/2; 74/3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Status: preliminary; translated from GB/EMBL/DDBJA;Molecule type: DNAA;Residues: 1-294 <MAG>
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C;Species: Caenorhabditis elegans
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999
C;Accession: T33588
R;Maggi, L.; Goela, D.
submitted to the EMBL Data Library, October 1998
A;Description: The sequence of C. elegans cosmid C40All.
                                                                                                                                                                                          A; Molecule type: mRNA
A; Residues: 1-304 <BEC>
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Listing first 45 summaries
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Fas ligand. Homo FasL/IT-alpha hybri FasL/IT-beta hybri FasL fusion constr FasL fusion constr FLAG peptide-Leuci Fas ligand (FasL) Non-cleavable Fas
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10-NOV-1993;
13-DEC-1993;
18-MAR-1994;
08-JUL-1994;
07-SEP-1994;
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                           Nagata S,
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ALIGNMENTS

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ligand; Tumour Necrosis factor family; apoptosis; cell cell surface antigen; human; Fas-L; CD179; truncated.
                                     MOCHIDA PHARM CO LTD. OSAKA BIOSCIENCE INST.
Nakamura N,
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93JP-0305975.
93JP-0342526.
94JP-0074344.
94JP-0180955.
94JP-0239363.
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Suda T,
Takahashi T;
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13-DEC-1993;
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08-JUL-1994;
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                           Sequence
                                          Fas ligands or active fragments able to induce apoptosis in which express the Fas cell surface antigen are claimed. The proteins are isolated from human, rat and mouse sources. The sequence represents part of the human Fas ligand.
                                                                                         Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI;
                                                                                                          Peptide which binds to Fas antigen, and for treatment and diagnosis of viral or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             are claimed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CD179 is a truncated human Fas ligand from which the Leu residue the C-terminus (position 179) has been deleted. Fas ligands able induce apoptosis in cells which express the Fas cell surface anti-
                                                                                                                                                                Nagata
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DB; AAQ94157.
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                            179
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Antigens derived from the present human Fas ligand sequence can be used in the preparation of a neutral antibody against an apoptosis inducing Fas ligand. The antibody can be used in a Fas ligand assay, e.g. an enzyme linked immunosorbant assay, to diagnose diseases in which the Fas ligand/Fas antigen system is implicated, e.g. hepatitis B/C, human immunodeficiency virus, graft/host disorders, ulcerative colitis or sequelae of myocardinfarction. The antibody may also be used to treat such diseases
                                                                                                                                                                                                                                                       Antibody reactive with Fas ligand capable of inducing apoptosis used for diagnostic assay of Fas ligand in body fluids and for treatment of diseases in which Fas ligand/Fas antigen is involved
                                                                                                                                                                                                            Disclosure; Fig 1; 164pp;
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30-JUN-1995;
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95JP-0188480
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60.72
/label- M54
79.89
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89..107
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47..60
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164..174
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Heteromeric complexes comprising lymphotoxin sub-units - us inhibitors of signalling by TNF- and TNF-related receptors, treating auto:immune disease, graft rejection. etc.
                                                                                                                           Browning
                                                                                                                                                                                                              07-JUN-1995;
                                                                                                                                                                                                                                                    06-JUN-1996;
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68..70
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172
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146
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Pred. No.
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                                                                                                                                                                                                                                            /note= ".
Misc-difference 129..130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C-terminal extracellular domain; CD40 ligand; mutated; trimerisation; lymphotoxin; LT; beta; alpha; tumour necrosis factor; TNF; inhibitor; signalling; receptor; Fas; treating; autoimmune disease; diabetes; rheumatoid arthritis; inflammatory bowel disease; HIV proliferation;
                                                                                                                                                                                                                                                                                        /note= "
Misc-difference 124..127
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177..17
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145..146
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92
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Pred. No. 0.055;
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ARBSGUT 6
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Best Local S
Matches 11
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                                                           30-DEC-1999;
                                                                                                                                                                                 DE19963859-A1
                                                                                                                                                                                                                                            Unidentified
                                                                                                                                                                                                                                                                                           Fusion protein; dimerization; oligomerization; Clq; vaccine; diphtheria; collectin; antiinflammatory; immunomodulatory; antiapoptotic; apoptotic; antiviral; antibacterial; antimalarial; antiprotozoal; antitumor; BCG; endocrinological; medicine; autoimmune disease; hyper-apoptotic state; hypor-apoptotic state; infection; tumor; endocrinological disorder; immunization; rubella; measles; poliomyelitis; rables; tetanus; malaria; yellow fever; human immune deficiency virus; influenza.
                                                                                                                      12-JUL-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Fast fusion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAB86306 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Heteromeric complexes comprising lymphotoxin sub-units - us inhibitors of signalling by TNF- and TNF-related receptors, treating auto:immune disease, graft rejection. etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (BIOJ ) BIOGEN INC
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   99DE-1063859
                                                           99DE-1063859
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Pred. No.
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CC bound signalling molecules or receptors or is an antibody (or its Cf fragment). The invention also describes (a) FP containing as component B CC a protein of the Ciq or collectin families; (b) DNA sequences (II) that CC cells containing the vector of (c); and (e) (II) in which component B of CC proteins. The products of the invention have antiinflammatory, antiprotozoal, antivinon have antiinflammatory antiprotozoal, antivimor and endocrinological activity. (I) CC are useful, in human or veterinary medicine, to: (i) produce pharmaceuticals for treatment of inflammation; autoimmune diseases; CC hyper- or hypo-apoptotic states; infections (particularly of the lymphatic system) and/or endocrinological disorders; (ii) produce vaccines for active or passive immunization against CC infections (specifically rubella, measles, poliowyselfitis, rables, CC virus or influenza), also as vaccine adjuvants; or (iii) for in vitro CC diagnosis. Crosslinking of component A is now achieved without requiring CC activity and regeneration of activity. This sequence represents the Fasi CC trimer construct described in the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This invention describes novel dimers or oligomers (1) of dl., tri. tetra or penta-mers (II) of recombinant fusion proteins (FP) comprising at least one each of components A and B, where A is a biologically active protein (or fragment) and B is a protein (or fragment) that causes
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  dimerization/oligomerization of (I) without requiring a third molecule. Particularly A functions as a ligand for antibodies, soluble or membrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     and component that induces oligomerization
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New dimers or oligomers of oligomeric recombinant fusion proteins, useful as pharmaceuticals and vaccines, comprises functional component
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (APOT-) APOTECH RES & DEV
  213
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  8
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RESULT 7 밁 AAB86307; AAB86307 standard; protein; 213 4 KELAELRESTS 51

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1 KELAELRESTS 11

Query Match
Best Local Similarity
Matches 11; Conserv

Conservative

0

100.0%;

Score 50; DB Pred. No. 0.0 0; Mismatches

DB 22 0.066; 22; 0

Length Indels

213; 0

Gaps

0

endocrinological; medicine; autoimmune disease; hyper-apoptotic st hypo-apoptotic state; infection; tumor; endocrinological disorder; immunization; rubella; measles; poliomyelitis; rabies; tetanus; ma Fusion protein; dimerization; oligomerization; C1q; vaccine; diphtheria; collectin; antiinflammatory; immunomodulatory; antiapoptotic; apoptotic; antiviral; antibacterial; antimalarial; antiprotozoal; antitumor; BCG; yerrow fever; human immune deficiency virus; influenza; super-FasL. malaria; state;

Fast fusion construct super-Fast.

13-SEP-2001

(first entry)

Unidentified

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RESULT 8
ABB05003
ID ABB0
XX
AC ABB0
XZ
AC ABB0
XX
PT 20-M
DT 20-M
XX
ELAG
XX
Huma
KW Huma
KW Liran
KW 11ve
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Homc
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Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This invention describes novel dimers or oligomers (I) of di-, tri-, tetra- or penta-mers (II) of recombinant fusion proteins (FP) comprising at least one each of components A and B, where A is a biologically active protein (or fragment) and B is a protein (or fragment) that causes dimerization/oligomerization of (I) without requiring a third molecule. Particularly A functions as a ligand for antibodies, soluble or membrane bound signalling molecules or receptors or is an antibody (or its fragment). The invention also describes (a) FP containing as component B a protein of the Clq or collectin families; (b) DNA sequences (II) that encode the FP of (a); (c) expression vectors containing (III); (d) host cells containing the vector of (c); and (e) (II) in which component B of FP is derived from the immunoglobulin, Clq or collectin families of proteins. The products of the invention have antiinflammatory, impurposed in the containing that is anticontaining the containing the vector of (c); and (e) (II) in which component B of the invention have antiinflammatory.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              immunomodulatory, antiapoptotic, apoptotic, antiviral, antibacterial, antimatory, antiapoptotic, apoptotic, antiviral, antibacterial, antimatarial, antiprotozoal, antitumor and endocrinological activity. (I) are useful, in human or veterinary medicine, to: (i) produce pharmaceuticals for treatment of inflammation; autoimmune diseases; hyper- or hypo-apoptotic states; infections (particularly viral); tumors (particularly of the lymphatic system) and/or endocrinological disorders; (ii) produce vaccines for active or passive immunization against infections (specifically rubella, measles, poliomyelitis, rabies, tetanus, diphtheria, BCG, malaria, yellow fever, human immune deficiency virus or influenza), also as vaccine adjuvants; or (iii) for in vitro diagnosis. Crosslinking of component A is now achieved without requiring a third molecule (e.g. antibody), resulting in increased biological activity and regeneration of activity. This sequence represents the super-Fast construct described in the method of the inventor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New dimers or oligomers of oligomeric recombinant useful as pharmaceuticals and vaccines, comprises and component that induces oligomerization -
                                                                  Human; Fas ligand; Fas ligand-fusion protein; leucine zipper; transmembrane protein; hepatotropic; immunosuppressive; apopt liver cell necrosis; viral hepatitis; autoimmune disease.
                                                                                                                                                                                                          FLAG peptide-Leucine zipper-human Fas ligand fusion protein.
                                                                                                                                                                                                                                                                                    20-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
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                                                                                                                                                                                                                                                                                                                                                          ABB05003
                                                                                                                                                                                                                                                                                                                                                                                                                            ABB05003 standard; Protein;
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11; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         213 AA;
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                                                                                                                                                                                                                                                                                (first entry)
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0.066;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 213;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   fusion proteins, functional component
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                   apoptosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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RESULT 9
AAY28597
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                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   which contains all or part of the Fas ligand sequence, a peptide capable of forming an oligomer and a peptide which increases the production yield of recombinant protein The fusion protein contains: (1) a FLAG peptide sequence; (2) an leucine zipper sequence; and (3) the extracellular domain of human Fas ligand. The fusion protein has hepatotropic and immunosuppressive activities. Binding of the Fas ligand sequence to Fas on the surface of cells expressing Fas induces apoptosis in the cells. The fusion protein can be used in the treatment of diseases with which Fas expressing cells are associated, such as liver cell necrosis produced by viral hepatitis, and autoimmune diseases. The present sequence represents a fusion protein of the present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             expression expressing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Fusion proteins of a Fas ligand with expression promoter peptide, useful f expressing Fas -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2002-097655/13.
N-PSDB; ABA92524.
                                                                                                                                                         Fas ligand; FasL; apoptosis; non-cleavable; graft intolerance; autoimmune destruction; cleavage site; mutein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 7; Page 46-48; 48pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Touma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Synthetic.
                                                                                   Misc-difference
                                                                                                                                                                                              Fas ligand (FasL) mutant delta
                                                                                                                                                                                                                       26-NOV-1999
                                                                                                                                                                                                                                              AAY28597;
                                                                                                                                                                                                                                                                       AAY28597 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (MOCH ) MOCHIDA PHARM CO LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26-MAY-2000; 2000JP-0156209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             28-MAY-2001; 2001WO-JP04456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      29-NOV-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO200190382-A2
                                             WO9936079-A1
                                                                                                                      Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             invention.
                                                                                                                                                                                                                                                                                                                                                                                             Local
                                                                                                                                                                                                                                                                                                                                   99
                                                                                                                                                                                                                                                                                                                                                           1 KELAELRESTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           present invention describes a fusion protein comprising a peptide
                                                                                                                                                                                                                                                                                                                                 KELAELRESTS
                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                   238
                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                   Æ
                                                                                   125..126
                                                                      /note= "Deletion of 20 wild-type amino acids (126-145)"
                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                    76
                                                                                                                                                                                                                                                                                                                                                           11
                                                                                                                                                                                                                                                                                                                                                                                              100.0%;
                                                                                                                                                                                                                                                                                                                                                                                    0
                                                                                                                                                                                                                                                                                                                                                                                             Score 50;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          for inducing
                                                                                                                                                                                                                                                                                                                                                                                              0.074;
                                                                                                                                                                                                                                                                                                                                                                                                          23;
                                                                                                                                                                                                                                                                                                                                                                                   0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          forming peptide and an apoptosis in cells
                                                                                                                                                                                                                                                                                                                                                                                                          Length 238;
                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                   0:
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07-JAN-1999;

99WO-US00667.

22-JUL-1999

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RESULT 10
AAW48954
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                                                                                                                                                                                                                                                                                                                                                                                                                                      This sequence is Fas ligand (FasL) mutant delta 3. This protein was made by deleting amino acids 126-145 (inclusive) of the wild-type FasL sequence AAY28594. The FasL protein activates the Fas receptor which induces apoptosis. The FasL deletion mutants (AAY28595-Y28597) are non-cleavable. The mutations inhibit the proteolytic cleavage of FasL and have the capacity to activate a Fas receptor-mediated pathway.

Claimed mutants of FasL or an organ or tissue expressing a mutant can be used to alleviate symptoms of a fas receptor-mediated pathway, such as the conseptoriate stimulation of a Fas receptor-mediated pathway, such as a poptosis, in a tissue or organ. In particular, FasL mutants protect to treat intolerance to a graft in a patient. The FasL mutants protect can organ or tissue from autoimmune destruction.

CC Note: The present sequence is not shown in the specification but it has been derived from the wild-type FasL sequence AAY28594 shown in the
                                                                                                                   Key
Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI;
           13-NOV-1997;
                              22-MAY-1998.
                                                                                      Reg1on
                                                                                                                                               Synthetic.
                                                                                                                                                          Homo
                                                                                                                                                                            glomerulonephritis.
                                                                                                                                                                                    Non-cleavable Fas ligand 1306145 deletion mutein; Fas; erythematosus; gene therapy; autoimmune disease; multiple sclerosis; rheumatoid arthritis; myasthenia gravis; transplant rejection;
                                                                                                                                                                                                                           Non-cleavable Fas ligand 1306145 deletion mutein.
                                                                                                                                                                                                                                               23-SEP-1998
                                                                                                                                                                                                                                                                                    AAW48954 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                    specification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 14; Page -; 81pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A non-cleavable Fas ligand polypeptide that has capacity to activate Fas receptor-mediated apoptosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Baekkeskov S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14-JAN-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (REGC ) UNIV CALIFORNIA
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                                                                                                                                                                                                                                                                                                                                   sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1999-468942/39
                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                               261
                                                                                                                                                                                                                                                                                                                                                                        100.0%;
ilarity 100.0%;
Conservative 0
                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Braat D,
           97WO-US20864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                98US-0006755
                                                                             130..265
/note= "r
                                                                                              /note= "represents residues 1-129 of the wild-type
Fas ligand"
                                                                                                                    Location/Qualifiers
1..129
                                                                                                                                                                                                                                                                                    Protein;
                                                                 represents residues 146-281 wild-type Fas ligand"
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Pred. No. 0.082;
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                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Stock PG;
                                                                                                                                                                                                                                                                                                                                                                                           Length 261;
                                                                                                                                                                                                                                                                                                                                                                         0;
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                                                                                                                                                                                                                                                                                                                 RESULT 11
AAW48953
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Best Local (
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                                                                                                                                     Key
Region
12-NOV-1997;
13-NOV-1996;
                            13-NOV-1997;
                                                                                                         Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Chu K;
                                                                                                                                                                  Synthetic.
                                                                                                                                                                                                                                                                                    AAW48953;
                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              rejection
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The present sequence represents a non-cleavable Fas ligand 1306145 deletion mutain. Fas ligand deletion mutein can be expressed in cells transfected with the DNA (AAV32623) coding for the mutant protein. These cells, expressing the mutant Fas ligand in a non-cleavable form, are claimed to be useful in vitro to identify cells that express Fas and, in vivo or in vitro, for reducing proliferation of Fas-expressing cells. The DNA encoding the Fas ligand mutant is claimed to be useful in gene therapy procedures and for the treatment of autoimmune diseases, e.g. multiple sclerosis, erythematosus, rheumatoid arthritis, glomerulonephritis, myasthenia gravis and transplant rejection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12-NOV-1997;
13-NOV-1996;
10-FEB-1997;
                                                                                                                                                                                                                                                                                                                                                                                                  glomerulonephritis.
                                                                                                                                                                                                                                                                                                                                                                                                                        gene therapy; rheumatoid ar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 4; Pages 65-66; 72pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1998-297861/26.
N-PSDB; AAV32623.
                                             22-MAY-1998
                                                                                           WO9821232-A2
                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Non-cleavable
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23-SEP-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New DNA encoding Fas ligand agonist including, e.g. deletion useful for, e.g. treating auto-immune diseases or transplant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Non-cleavable
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         109 KELAELRESTS 119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CHIRON
                                                                                                                                                                                                                                                                                                                                                                                                                   ble Fas ligand 1306142 deletion mutein; Fas; erythematosus; py; autoimmune disease; multiple sclerosis; arthritis; myasthenia gravis; transplant rejection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%;
milarity 100.0%;
Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  265 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Fas ligand 1306142 deletion mutein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   97US-0968686.
96US-0030871.
97US-0039972.
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97WO-US20864
                                                                                                                                                                                      130..268
                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                      "represents residues 143-281 of wild-type Fas ligand"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0
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Pred. No. 0.0
); Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               19;
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97US-0968686 96US-0030871

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           These cells, expressing the mutant Fas ligand in a non-cleavable form, are claimed to be useful in vitro to identify cells that express Fas and, in vivo or in vitro, for reducing proliferation of Fas-expressing cells. The DNA encoding the Fas ligand mutant is claimed to be useful in gene therapy procedures and for the treatment of autoimmune diseases, e.g. multiple sclerosis, erythematosus, rheumatoid arthritis, glomerulonephritis, myasthenia gravis and transplant rejection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present sequence represents a non-cleavable Fas ligand 1306142 deletion mutein. Fas ligand deletion mutein can be expressed in cells transfected with the DNA (AAV22622) coding for the mutant protein.
                                                                                                                                                                                                                                                     Homo sapiens
Synthetic.
                                                                                                                                 07-JAN-1999;
                                                                                                                                                                                                                                                                                                    Fas ligand;
                                                                                                                                                                                                                                                                                                                          Fas ligand (FasL) mutant delta
                                                                                                                                                                                                                                                                                                                                                   26-NOV-1999
                                                                                                                                                                                                                                                                                                                                                                         AAY28596
                                                                                                                                                                                                                                                                                                                                                                                                AAY28596 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 4; Pages 62-63; 72pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New DNA encoding Fas ligand agonist including, e.g. deletion useful for, e.g. treating auto-immune diseases or transplant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N-PSDB; AAV32622
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HPI;
                                    WPI; 1999-468942/39
                                                                                  (REGC ) UNIV CALIFORNIA
                                                                                                         14-JAN-1998;
                                                                                                                                                        22-JUL-1999
                                                                                                                                                                               W09936079-AJ
                                                                                                                                                                                                                   Misc-difference
                                                                                                                                                                                                                                                                                         autoimmune destruction;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10-FEB-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (CHIR ) CHIRON CORP
non-cleavable Fas ligand polypeptide as receptor-mediated apoptosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 KELAELRESTS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1998-297861/26
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        268 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%;
ilarity 100.0%;
Conservative (
                                                                                                                                                                                                                                                                                      FasL; apoptosis; non-cleavable; graft intolerance;
destruction; cleavage site; mutein.
                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                         98US-0006755
                                                                                                                                 99WO-US00667
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                                                          Braat D,
                                                                                                                                                                                                                Location/Qualifiers 125..126
                                                                                                                                                                                                       /note=
                                                                                                                                                                                                                                                                                                                                                                                                Protein; 271
                                                                                                                                                                                                    *Deletion of 10 wild-type amino acids
                                                          Kang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        <u>;</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 50;
Pred. No.
                                                          ŝ
                                                                                                                                                                                                                                                                                                                          2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                          Stock
         that has capacity to activate
                                                          မှ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0.085;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 19;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
                                                                                                                                                                                                     (126-135)"
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RESULT 13
AAY28595
ID AAY28
XX AAY28
XX AAY28
AC Fas 1
XX Fas 1
KW Fas 1
KW Fas 1
KW Fas 1
KW AUTOI
XX Homo
OS Synt!
XX Exam
OS Seque
CC This
CC Seque
CC Sequ
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           and have the capacity to activate a Fas receptor-mediated pathway. Claimed mutants of Fasl or an organ or tissue expressing a mutant can be used to alleviate symptoms of a disorder characterized by inadequate or inappropriate stimulation of a Fas receptor-mediated pathway, such as apoptosis, in a tissue or organ. In particular, Fasl mutants can be used to treat intolerance to a graft in a patient. The Fasl mutants protect an organ or tissue from autoimmune destruction.

Note: The present sequence is not shown in the specification but it has been derived from the wild-type Fasl sequence AAY28594 shown in the
  This sequence is Fas ligand (Fast) mutant delta 1. by deleting amino acids 126-129 (Inclusive) of the sequence AAY28594. The Fast protein activates the induces apoptosis. The Fast deletion mutants (AAY28
                                                                                                                                                                 A non-cleavable Fas ligand polypeptide Fas receptor-mediated apoptosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Fas ligand;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                specification.
                                                                                                                          Example
                                                                                                                                                                                                                                                                                       Baekkeskov S,
                                                                                                                                                                                                                                                                                                                                   (REGC ) UNIV
                                                                                                                                                                                                                                                                                                                                                                                  14-JAN-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           autoimmune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Fas ligand (FasL) mutant delta 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              26-NOV-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAY28595;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAY28595 standard; Protein; 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            109
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 KELAELRESTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Loca 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KELAELRESTS
                                                                                                                                                                                                                                             1999-468942/39
                                                                                                                     1; Page -; 81pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Page -; 81pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           destruction;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FasL;
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                                                                                                                                                                                                                                                                                       Braat D,
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125..126
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           apoptosis; non-cleavable; graft intolerance;
ction; cleavage site; mutein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Deletion of 4 wild-type
                                                                                                                     English.
                                                                                                                                                                                                                                                                                       Kang
-129 (inclusive) of the wild-type Fast protein activates the Fas receptor which deletion mutants (AAY)ARSGR-V20FAR.
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 20
0.086;
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Best Local
                                                        The present sequence is a protease-resistant Fas ligand derivative in which a region of human Fas ligand which is susceptible to protease attack has been deleted. The present invention also describes appprosis modulators containing soluble Fas ligand. The modification in the Fas ligand renders it resistant to the action of proteases such as the metalloproteinase which in vivo cleaves the active membrane-bound Fas ligand (which is active as an apoptosis inducer). The Fas ligand can be used for the prevention and treatment of diseases such as cancer, viral infection and autolimune disease, e.g. by introduction of DNA encoding the modified Fas ligand into effector cells using a suitable gene
                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 4; Page 48-49; 60pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1999-229531/19.
N-PSDB; AAX33117.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            non-cleavable. The mutations inhibit the proteolytic cleavage of FasL and have the capacity to activate a Fas receptor-mediated pathway. Claimed mutants of FasL or an organ or tissue expressing a mutant can be used to alleviate symptoms of a disorder characterized by inadequate or inappropriate stimulation of a Fas receptor-mediated pathway, such as apoptosis, in a tissue or organ. In particular, FasL mutants can be used to treat intolerance to a graft in a pathent. The FasL mutants protect an organ or tissue from autoimmune destruction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Protease-resistant Fas ligand derivatives used for prevention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
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en derived from the wild-type FasL sequence AAY28594 shown
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OSAKA BIOSCIENCE
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l1; Conservative
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Pred. No.
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RESULT 15
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                                                                       Sequence
                                                                                         expressed
                                                                                                 screened with a murine Fas-L probe. Isolated clones were amplified by PCR, and a desired fragment ligated into vector pBluescript SK. The cDNA insert of recombinant vector Fas-L/pBs, deposited as E. coli ATCC 69527, is given in AAQ91311. Recombinant Fas-L was
                                                                                                                                       A cDNA library prepd. from human peripheral blood lymphocyte mRNA was
                                                                                                                                                       Claim 3; Page 25-27; 38pp; English.
                                                                                                                                                                                  Human and murine DNA encoding ligand(s) binding to cell surface protein Fas - useful for studying auto-immune disorder(s) and development of
                                                                                                                                                                                                             N-PSDB; AAQ91311.
                                                                                                                                                                                                                       WPI; 1995-255032/33
                                                                                                                                                                                                                                         Goodwin
                                                                                                                                                                                                                                                                             01-FEB-1994;
07-JAN-1994;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Fas ligand; Fas-L;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human Fas-L protein
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          KELAELRESTS 11
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94US-0179138.
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/label= Transmembrane_domain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cell surface protein; autoimmune disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Protein;
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KELAELRESTS 119

Search completed: March 13, 2003, 18:49:12 Job time: 30.2 secs

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Result
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                                                                                                                                                                                                                                                                                                                          Pred. No. is the number of results predicted by chance to have score greater than or equal to the score of the result being and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                             Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    seq length:
seq length:
      44444444
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Gapop 10.0 , Gapext 0.5
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                                                                                                                                                                                                                             Match
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    17:11:10:
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0. /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1988 DAT: *
11. /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1990 DAT: *
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18. /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1999 DAT: *
19. /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1990 DAT: *
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10. /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1990 DAT: *
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/SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1982.DAT:*
/SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1983.DAT:*
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ABB917961
ABB9179118
AAU75795
ABP17190
AAU90096
ABB96233
AAW36881
ABP17219
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Protease peptide.
Human immunodefici
HIV B27 super moti
Human cathepsin S
Substrate for cath
HIV protease cleav
HIV B27 super moti
                                                                                                                                                                                                                         Description
                                                                                                                                         HIV A02 super moti
HIV B58 super moti
Cathepsin S inhibi
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172	100	97	69	69	40	36	36	34	34	34	34	34	34	34	34	34	34	34	32	32	32	32	32	30	25	15	15	15	15	15		15		12
14	17	22	12	12	17	16	16	20	20	20	20	19	19	18	18	16	16	16	20	20	19	18	16	23	19	22	22	20	20	19	18	16	13	22
AAR43240	AAW03357	AAB67383	AAR14459	AAR14009	AAW03358	AAR77757	75	AAW99903	AAW98895	AAY39723	AAY39722	AAW67393	AAW67392	AAW25876	AAW25877	AAR77726	AAR68707	70	AAW99970	AAY39767	AAW67362	AAW25846	AAR68676	AAU84422	AAW82529	ABP24915	ABP24909	AAW98894	AAY39674	AAW67391	AAW25875	AAR68705	563	ABP17220
Gag sequence. Hum	Human immundeficie	p24c DNA. Human i		HIV-1 hxb2 gag 318	efi		P24M/CLTB-56 chime	æ	HIV-1 vaccine synt	HIV1 chimeric pept	chimeric				Chimaeric T/B cell	P24M/V3 consensus	CLTB-56/P24M chime	P24M/CLTB-56 chime		per		Chimaeric T/B cell	3		-1 p24 epitop	mot1f	mot	n		m	æ	itope, P	4	HIV B27 super moti

ALIGNMENTS

RESULT 1 ABP12751

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THE STANCE OF TH
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Baker DM,
Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1) peptide groups, useful for vaccinating against HIV-1 -
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                                                                                                                                                                                                                                                                                                                                                                                                  (EPIM-) EPIMMUNE INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   05-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              05-OCT-2000; 2000WO-US27766
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human immunodeficiency virus type 1.
                                                                                                                                                                                                                                               Sidney J,
Celis E,
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Kubo RT, Grey
                                                                                                                                                                                                                                                                                                 Livingston BD,
                                                                                                                                                                                                                                                         HM;
                                                                                                                                                                                                                                                                                                 Chesnut
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HIV; HIV-1; human immunodeficiency virus; env; pol; gag; nef; vpr; vpu; vif; tat; cytotoxic T lymphocyte; CTL; immune response; epitope; antigen; vaccine; HIV infection; immunisation; virucide.

HIV A02 super motif gag peptide #222.

15-JUL-2002 (first entry)

ABP12751;

ABP12751 standard; Peptide; 9

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Claim

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RESULT 2
ABP17961
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        compositions immunodeficiency virus-1 (HIV-1) group comprising an anino acid sequence selected from 51 defined anino acid sequences (ABL25347 to ABP25397). (I) has virucide activity and can be used in vaccines. (I) comay be used for immunising subjects against HIV-1 infections. The use of group-based vaccines has several advantages over traditional vaccines, compositions. There is evidence that the immune response to whole compositions. There is evidence that the immune response to whole callowing for immune escape due to mutations. The groups for inclusion in group-based vaccine may be selected from conserved regions of viral or compositions. Furthermore, immunessive groups for inclusion in group-based vaccine may be selected from conserved regions of viral or timmuna response to antigens, which therefore reduces the likelihood of cessape mutants. Furthermore, immunosuppressive groups that may be present in whole antigens can be avoided with the use of group-based vaccines. An additional advantage of an group-based vaccine approach is the ability to combine selected groups, achieving, for example, enhanced immunogenicity. Accordingly, the immune response can be modulated, as a propriate, for the target disease. Similar engineering of the response can be petide sequences used in the exemplification of the present convention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
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               Claim 32; Page 237; 448pp; English
                                                                                                                                  Sette
Baker
                                                                                                                                                                                                                                                                                                                                                                                      HIV; HIV-1; human immunodeficiency virus; env; pol; gag; nef; vpr; vpu; vif; tat; cytotoxic T lymphocyte; CTL; immune response; epitope; antigen; vaccine; HIV infection; immunisation; virucide.
                                             Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1) peptide groups, useful for vaccinating against HIV-1 -
                                                                                                                                                                                                                      05-OCT-1999;
                                                                                                                                                                                                                                                     05-OCT-2000; 2000WO-US27766
                                                                                                                                                                                                                                                                                        12-APR-2001
                                                                                                                                                                                                                                                                                                                                                         Human immunodeficiency virus type 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       HIV B58 super motif gag peptide #180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                     (EPIM-) EPIMMUNE INC
                                                                                                                                                                                                                                                                                                                       WO200124810-A1
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                                                                                                   2001-354887/37.
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9; Conserv
                                                                                                                                  Sidney J,
Celis E,
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                                                                                                                                                                                                                    99US-0412863.
                                                                                                                                  Southwood S, Livingston BD, Kubo RT, Grey HM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            88.9%; Score 40;
100.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 22; 1
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                                                                                                                                                    Chesnut
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RESULT 3
ABB80017
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Best Local (
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                                                                                                                                                                                                                                                                                                                                                                                                             Cathepsin S; antiallergic; antiasthmatic; dermatological; pyrazole; atopic allergy; hay fever; asthma; atopic dermatitis; food allergy; allergy; dust; pollen; mold; pet dander; pet hair.
                                                                                                                                                                      06-SEP-2000; 2000US-230407P.
10-AUG-2001; 2001US-0927324.
                                                                                                                                                                                                                                                                                                                                 Key
Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cathepsin S inhibition assay substrate peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17-JUL-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABB80017 standard; peptide; 10
                                            WPI; 2002-393814/42.
                                                                         Karlsson L, Khatuya H,
Tays KL, Thurmond RL,
                                                                                                          Butler CR,
                                                                                                                                                                                                                      05-SEP-2001; 2001WO-US27429
                                                                                                                                                                                                                                                      14-MAR-2002.
                                                                                                                                                                                                                                                                                                                                                                                 Unidentified
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                                                                                                                                       (ORTH ) ORTHO-MCNEIL PHARM INC
                                                                                                                                                                                                                                                                                    WO200220011-A2
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9; Conserv
                                                                                                        Cai H,
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                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
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                                                                                                        Edwards JP,
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100.0%; Pr
                                                                         Meduna
Wei J;
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Pred. No.
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                                                                                         SP,
                                                                                           Grice CA, (
SP, Pio BA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 22;
7.8e+05;
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                                                                                           Sehon CA, S
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Treatment of allergic conditions e.g. atopic dermatitis or asthma comprises administration of pyrazole derivative that inhibits cathepsin

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RESULT 4
AAE19118
ID AAE1
AXX AAE1
AXX AAE1
AXX AAE1
AXX AAE1
AXX AAE1
AXX Luci
KW cell
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"---hes 9; Conserv
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                      The invention relates to a purified polypeptide having luciferase activity and a recognition site specifically cleavable by a protease, where cleavage results in a decrease in luciferase activity. The polypeptide comprises a localisation sequence which is linked to the luciferase polypeptide by the cleavable recognition sequence. The polypeptide is useful for identifying a protease (Caspase-3) activity modulator, an inhibitor of apoptosis and for detecting luciferase activity in a sample. The polypeptide is used for characterising and identifying cellular processes associated with metabolism, cell growth and cell death e.g. apoptosis and for measuring protease activity. The protease measurement methods are useful for characterising, identifying cellular biochemical pathways as well as identifying diagnostic and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New purified luciferase polypeptide, useful for identifying protease activity modulators, comprises recognition site cleavable by protease, where cleavage of polypeptide results in decreased luciferase activity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to the treatment of allergic conditions, comprising the administration of a pyrazole derivative. The activity of derivatives of the invention may be described as, antiallergic, antiasthmatic and dermatological. They act as cathepsin S inhibitors and may be used for the treatment of allergic conditions including atopic allergies, e.g. hay fever, asthma, atopic dermatitis, food allergies and allergies to dust, pollen, mold, pet dander or pet hair. The current sequence represents a cathepsin S inhibition assay substrate peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cell death.
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                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 63; Page
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19-JUL-2000; 2000US-0619047
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21-MAY-2002 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (CHEM-) CHEMICON INT INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 EKARVLAEA 9
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for modulating diseases or disorders associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            enzyme;
                                                                                                                                                                                                                                                                                                                                                                                                                                              24;
                                                                                                                                                                                                                                                                                                                                                                                                                                       56pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          peptide; 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        protease; cell growth; apoptosis; therapeutic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                88.9%;
100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        English.
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0.13;
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Best Local Similarity
Best 5 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ρy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       biochemical pathways. The polypeptide is also useful as a substratuse study agents or conditions that cleave the recognition site and for determining amount of protease in a sample and for monitoring the activity of protease inside a cell that expresses a recombinant luciferase. The present sequence is a protease peptide used in the
          The present invention relates to a new nucleic acid construct that comprises a polynucleotide cassette encoding a chimeric polypeptide. The chimeric polypeptide comprises a first polypeptide sequence, a second polypeptide sequence translationally fused to the first sequence, and a protease recognition site (PRS) cleavable by a virally encoded protease, where cleavage of the PRS leads to a detectable signal. The nucleic acid construct of the invention is useful for uncovering molecules having antiviral activity or for determining viral drug resistance and the chimeric peptide is also useful for detecting the presence of a virus in a cell. Other uses of the invention are detecting viral encoded protease found in infected cells or detecting the presence of viral infection. The nucleic acid construct is useful for phenotypic testing of human immunodeficiency virus (HIV) drug resistance.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human immunodeficiency virus Gag protein protease cleavage sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  08-MAY-2002
                                                                                                                                                                                                                                                                         New nucleic acid construct for detecting anti-viral drugs, comprises polynacleotide cassette encoding a chimeric polypeptide with two polypeptide sequences and—a protease recognition site cleavable by a virally encoded protease
                                                                                                                                                                                                                                                                                                                                                                                                                                                           31-JUL-2000; 2000US-0629969.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gag protein; antiviral; nucleic acid construct; viral protease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         30-JUL-2001; 2001WO-IL00702
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cleavage-site
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAU75795;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAU75795 standard; Peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             invention.
                                                                                                                                                                                                                                           Example 1; Page 32; 93pp; English.
                                                                                                                                                                                                                                                                                                                                                           WPI; 2002-188753/24
                                                                                                                                                                                                                                                                                                                                                                                                                          (AMID-) AMIDUT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           07-FEB-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   protease recognition site;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 KARVLAEAM 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /label- HIV_protease_cleavage_site
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   viral drug
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0.13;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   resistance; HIV;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0
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C
CC human immunodeficiency virus-1 (HIV-1) group comprising an amino acid corequence selected from 51 defined amino acid sequences (ABL25347 to CC ABP25397). (I) has virucide activity and can be used in vaccines. (I) CC may be used for immunising subjects against HIV-1 infections. The use of group-based vaccines has several advantages over traditional vaccines, CC particularly when compared to the use of whole antigens in vaccine cc compositions. There is evidence that the immune response to whole cantigens is directed largely toward variable regions of the antigen, CC allowing for immune escape due to mutations. The groups for inclusion in CC an group-based vaccine may be selected from conserved regions of viral or cescape mutants. Furthermore, immunosuppressive groups that may be present in whole antigens can be avoided with the use of group-based vaccines.

CC An additional advantage of an group-based vaccine approach is the ability the
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Baker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HIV; HIV-1; human immunodeficiency virus; env; pol; gag; nef; vpr; vpu; vif; tat; cytotoxic T lymphocyte; CTL; immune response; epito antigen; vaccine; HIV infection; immunisation; virucide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           and allows efficient detection of the presence of viral protease and viral particles within cells. The construct is specific, sensitive and lacks background enzymatic activity in the absence of human immunodeficiency virus protease, and is suitable for detection of specific viral strain isolates even under low viral load conditions. Whe used for phenotypic testing of HIV drug resistance it delivers accurate results within 24 hours. The present amino acid sequence represents one of several (AAU75794-AAU75798) HIV Gag protein protease cleavage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (EPIM-)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HIV B27 super mot1f gag peptide #66.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABP17190
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         present invention describes a composition (I) comprising
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9; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                compositions
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sidney J,
Celis E,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 that were used in the invention for HIV detection.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     221; 448pp;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Southwood S, I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              comprising human immunodeficiency if for vaccinating against HIV-1 -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             virus-1 (HIV-1)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         a prepared
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        composition of the groups, achieving, for example, enhanced immunogenicity. Accordingly, the immunogenicity accordingly, the immunogenicity accordingly, the immunogenicity accordingly the instance of the response appropriate, for the target disease. Similar engineering of the response is not possible with traditional approaches. ABP11501 to ABP25412 represent peptide sequences used in the exemplification of the present
                                                                                                                    Treating allergic conditions, e.g. hay fever, and food allergies, comprises administration (
                                                                                                                                                                                                             06-SEP-2000;
10-AUG-2001;
                                                                                                                                                                                                                                                                                                                                                                        Synthetic
                                                                                         Example 37; Page 92; 115pp; English
                                                                                                                                                WPI; 2002-527344/56
                                                                                                                                                                  Thurmond
                                                                                                                                                                           Cai H,
                                                                                                                                                                                            (ORTH ) ORTHO-MCNEIL PHARM INC
                                                                                                                                                                                                                                          05-SEP-2001;
                                                                                                                                                                                                                                                           14-MAR-2002
                                                                                                                                                                                                                                                                                                         Modified-site
                                                                                                                                                                                                                                                                                                                           Modified-site
                                                                                                                                                                                                                                                                                                                                                      Key
                                                                                                                                                                                                                                                                                                                                                                                                   Cathepsin S;
                                                                                                                                                                                                                                                                                                                                                                                                                    Human cathepsin S substrate peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                       24-SEP-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAU80096;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAU80096 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  invention
                                                                                                                                                                                                                                                                              WO200220013-A2
                                                                                                                                                                                                                                                                                                                                            Modified-site
                                                                                                                                                                                                                                                                                                                                                                                          food allergy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 KARVLAEAM 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KARVLAEAM 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
9; Conser
                                                                                                                                                                 Edwards JP,
1 RL, Wei J;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                             2000US-230407P
2001US-0927188
                                                                                                                                                                                                                                                                                                                                                                                                   allergy; pyrazole; hay fever; asthma; atopic dermatitis;
                                                                                                                                                                                                                                         2001WO-US27480
                                                                                                                                                                                                                                                                                                                                                                                                                                       (first
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                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                /label= C-terminal
                                                                                                                                                                                                                                                                                                                  /note=
                                                                                                                                                                                                                                                                                                                                    /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                       entry)
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                                                                                                                                                                                                                                                                                                                                    "Aedens-Glu"
                                                                                                                                                                                                                                                                                                                  "Dabcyl"
                                                                                                                                                                           Karlsson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0
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Pred. No.
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0.15;
                                                                                                                                                                            Meduna
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              22;
                                                                                                                   of a substituted pyrazole
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0,
                                                                                                                                                                           SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length
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The invention relates to a method of treating allergic conditions comprising administration of a composition comprising a substituted pyrazole (I) or a salt, amide or learning an accompanient of the method is used for treating allergic conditions, e.g. hay fever, asthma, atopic dermatitis and food allergies. The present sequence represents human cathepsin S substrate peptide used in an assay to demonstrate the method of the

Sequence

11

Invention

Length 11

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RESULT 8
ABB76233
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                                                                                          The present sequence is a peptide used as substrate for a cathepsin S inhibition assay. The km for the substrate is around to be under the presence of substrate inhibition makes kinetic analysis difficult. With 20 uM substrate, the assay rate is linear over the range of 1-8 ng cathepsin S in 100 ul reaction. Using 2 ng/well of cathepsin S, the production of product is linear and yields about 7-fold signal after 20 min with only 20% to 10ss of substrate. Primary assays are run by quenching the reaction after 20 min and then measuring the fluorescence. For other assays, measurements are taken every min for 20 min. The rate is calculated from the slope of the increase and the percent inhibition is calculated from this. The present invention relates to the use of cathepsin S inhibitors to treat an allergic condition, especially an atopic dermatitis or a food allergy such as hay fever, asthma, atopic dermatitis or a food allergy. The allergens may include dust, pollen, mould, and pet
    Query Match
Best Local Similarity
Matches 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cathepsin S; inhibitor; allergy; hay fever; asthma; food allergy; atopic dermatitis; antiallergic; antiasthmatic; dermatological;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Substrate for cathepsin S inhibition assay.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            09-AUG-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABB76233;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABB76233 standard;
                                                                                                                                                                                                                                                                                                                                                      Use of cathepsin S inhibitor for treating hay fever, asthma, atopic dermatitis or a
                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2002-443877/47.
                                                                                                                                                                                                                                                                                                                                                                                                                          Gu Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              06-SEP-2000; 2000US-230407P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         05-SEP-2001; 2001WO-US27441.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            antiinflammatory; immunosuppressive.
                                                          Sequence
                                                                                                                                                                                                                                                                                                                             Example 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    (ORTH ) ORTHO-MCNEIL PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   \vdash
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                                                                                   pet
                                                                                                                                                                                                                                                                                                                           Page
                                                          11 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                       ۳
                                                                                                                                                                                                                                                                                                                           29; 53pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note= "Aedens-glutamic acid"
11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note= "Dabcyl lysine-amide"
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88.9%; 5c.
100.0%; Pro
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                                                                                                                                                                                                                                                                                                                           English.
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Pred. No.
                Score 40; DB 23;
Pred. No. 0.15;
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      Mismatches
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. 0.15;
                                                                                                                                                                                                                                                                                                                                                    an allergic condition, food allergy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0
     0
                           Length 11;
      Indels
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    0;
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     Gaps
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RESULT 10 ABP17219 ID ABP17

ABP17219 standard; Peptide; 12

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RESULT 9
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                                                                                                                                                                 of a ricin-like protein in a novel recombinant protein. A nucleic acid (see AAT97900) encoding such a construct is obtained by PCR mutagenesis of the wild-type ricin linker sequence. The invention provides novel recombinant proteins which incorporate the A and B chains of a ricin-like toxin (preferably the A and B chains of ricin) linked by a heterologous linker sequence containing a ricin linked by a heterologous linker sequence containing a roteleavage recognition site for a retroviral protease such as HIV protease (see AAM36880-82), HTLV-I (see AAM36883-43) or HTLV-II (see AAW36885-65). The recombinant proteins selectively inhibit or destroy mammalian cells infected with a retrovirus such as cancer cells associated with HTLV or cells associated with HTLV. The recombinant proteins are non-toxic until the ricin A chain is liberated from the B chain by a retroviral protease, and thus can be used to specifically target infected cells without the need
                                                          Best Loc
Matches
                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DNAs encoding ricin like toxins A and B - are linked v containing cleavage site for retroviral protease, used destroy mammalian cells infected with retrovirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAW36881;
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                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                           This claimed peptide is a cleavage recognition site for a HIV protease. It is utilised as a linker between the A and B chains
                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 5; Page 41; 105pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1997-549735/50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Borgford T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (CANG-) CANGENE CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     30-APR-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   29-APR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  06-NOV-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 W09741233-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AIDS; infection; therapy; linker.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ricin; toxin; antiviral; virucide; retrovirus; protease; HIV;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HIV protease cleavage recognition site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11-MAY-1998
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                                                          Local Similarity
hes 9; Conserv
2 KARVLAEAM 10
                          2 KARVLAEAM 10
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                                                                                                                                                      cell
                                                                                                                                                    to specifically target infected ell binding component.
                                                                                                                       12 AA;
                                                          88.9%; Score 40; llarity 100.0%; Pred. No. Conservative 0; Mismatc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    97WO-CA00288
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                                                            Mismatches
                                                                         DB 18;
0.16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        are linked via linker
otease, used to inhibit or
                                                            0,
                                                                                         Length 12;
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                                                            Gaps
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RESULT 11
ABP17220
ID ABP17
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AC ABP17
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                                                                                                                                                                                                                                                                                                   The present invention describes a composition (1) comprising a prepared CC human immunodeficiency virus-1 (HIV-1) group comprising an amino acid companies as elected from 51 defined amino acid sequences (BHI25347 to CC ABP23397). (I) has virucide activity and can be used in vaccines. (I) cmay be used for immunising subjects against HIV-1 infections. The use of CC group-based vaccines has several advantages over traditional vaccines. (CC particularly when compared to the use of whole antigens in vaccine CC compositions. There is evidence that the immune response to whole CC antigens is directed largely toward variable regions of the antigen in CC allowing for immune escape due to mutations. The groups for inclusion in CC tumour-associated antigens, which therefore reduces the likelihood of CC tumour-associated antigens, which therefore reduces the likelihood of CC escape mutants. Furthermore, immunosuppressive groups that may be present CC in whole antigens can be avoided with the use of group-based vaccines. (CC and additional advantage of an group-based vaccine approach is the ability CC composition of the groups (CTL and HTL), and further, to modify the CC composition of the groups, achieving, for example, enhanced CC immunogenicity. Accordingly, the immune response can be modulated, as appropriate, for the target disease. Similar engineering of the response CC invention.
                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                       Query Match
Best Local :
                 ABP17220
                                               ABP17220 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1) peptide groups, useful for vaccinating against HIV-1 -
                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 32; Page 221; 448pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2001-354887/37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Baker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           05-OCT-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO200124810-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human immunodeficiency virus type 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (EPIM-) EPIMMUNE INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HIV B27 super motif gag peptide #95
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                                                                                                                                                                                                       Local Similarity
nes 9; Conser
                                                                                                                                        4
                                                                                                                                                           2 KARVLAEAM 10
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|KARVLAEAM 12
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Celis E,
                                                                                                                                                                                                                                                                         12
                                                                                                                                                                                                     Conservative
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                                                 Peptide; 12 AA.
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                                                                                                                                                                                                                     88.9%; Score 40; 100.0%; Pred. No.
                                                                                                                                                                                                     0
                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                     DB 22;
0.16;
                                                                                                                                                                                                     0
                                                                                                                                                                                                                                     Length 12;
                                                                                                                                                                                                     Indels
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RESULT 12
AAR25633
ID AAR25
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AC AAR25
XX
AC AAR25
XX
DT 17-DE
DT 19-JA
XX
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Best Local Similarity
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                                                                                                                                                                                                                                        Ş
                                                                                                                                                                                                                                                                                                                                                           The present invention describes a composition (I) comprising a prepared CC human immunodeficiency virus-I (HIV-I) group comprising an amino acid companies and composition and acid composition acid companies are companied in vaccines. (I) CC abp25397). (I) has virucide activity and can be used in vaccines. (I) CC may be used for immunising subjects against HIV-I infections. The use of group-based vaccines has several advantages over traditional vaccines, cc particularly when compared to the use of whole antigens in vaccine CC compositions. There is evidence that the immune response to whole compositions of the antigen, and in a directed largely toward variable regions of the antigen, cc antigens is directed largely toward variable regions of the antigen, cc allowing for immune escape due to mutations. The groups for inclusion in cc an group-based vaccine may be selected from conserved regions of viral or cc an agroup-based vaccines the likelihood of cescape mutants. Furthermore, immunosuppressive groups that may be present in whole antigens can be avoided with the use of group-based vaccines. CC an additional advantage of an group-based vaccine approach is the ability composition of the groups (CTL and HTL), and further, to modify the cc composition of the groups, achieving, for example, enhanced composition of the groups, achieving, for example, enhanced composible with traditional approaches. ABP11501 to ABP5412 createsent neartific action of the response can be modulated, as a proposition of the capen and the propose can be modulated.
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Baker DM,
                                                                                                            AAR25633 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1) peptide groups, useful for vaccinating against HIV-1 -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HIV; HIV-1; human immunodeficiency virus; env; pol; gag; nef; vpr; vpu; vif; tat; cytotoxic T lymphocyte; CTL; immune response; epitope; antigen; vaccine; HIV infection; immunisation; virucide.
                                                                         AAR25633;
                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 32; Page 221; 448pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2001-354887/37.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     05-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        05-OCT-2000; 2000WO-US27766
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human immunodeficiency virus type 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HIV B27 super motif gag peptide #96.
                                                                                                                                                                                                                                                                                                                                                                                                               represent peptide sequences used in the exemplification of the present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (EPIM-) EPIMMUNE INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12-APR-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO200124810-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15-JUL-2002 (first entry)
                                                                                                                                                                                                         4 KARVLAEAM 12
                                                                                                                                                                                                                                          2 KARVLAEAM 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sidney J,
Celis E,
                                                                                                                                                                                                                                                                                                                                                           12 AA;
                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9905-0412863
                                                                                                              Protein; 14
                                                                                                                                                                                                                                                                                                 88.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Southwood Kubo RT,
                                                                                                                                                                                                                                                                                 0;
                                                                                                                                                                                                                                                                                                   Score 40;
; Pred. No.
                                                                                                              B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        S, Livingston Grey HM;
                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                 DB 22
0.16;
                                                                                                                                                                                                                                                                                                                    22;
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                                                                                                                                                                                                                                                                                                                  Length 12
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                                                                                                                                                                                                                                                                                 Gaps
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17-DEC-2001 19-JAN-1993

(updated)
(first entry)

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RESULT 13
AAR68705
ID AAR68
XX AAR68
XX AAR68
XX O7-SE
DT 07-SE
XX T-Cel
XX T-Cel
XX Gpl60
XX
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The sequences given in AAR25632-38 are peptides which are hydrolysed.

C by aspartyl proteinase (AP) in the assay of the invention. These peptides have labelled C-terminal portions which are polar. These portions are separated from the unlabelled hydrophobic w-terminal portions by hydrolysis by AP. Following hydrolysis of these peptides with AP, the hydolysed polar portion is separated from the unhydrolysed polypetide and the amount of hydrolysed polypeptide determined. This assay can be used to detect inhibitors of AP with potential as therapeutic agents, eg. for treating AIDS. This assay has a higher sensitivity than previous methods.

(Note: Revised entry submitted to correct the patent number format of US Government-owned NTIS applications to prevent classes with ongoing US granted patent numbers. For further information please visit the Derwent we web site at www.derwent.com/dwpi/updates/ntis_us.html.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                            T-cell; epitope;
gpl60; gag; pol;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Assay for retroviral aspartyl proteinase - provides rapid accurate and inexpensive method for detecting aspartyl proteinase inhibitors, e.g. for AIDS treatment
                                                                                                                                                                                                                                                                                                  07-SEP-1995
                                                                                                                                                                                                                                                                                                                                                    AAR68705
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Page 10; 27pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Knight M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15-APR-1992.
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                                                                                                          Human immunodeficiency virus
                                                                                                                                                                                                                                                                                                                                                                                                         AAR68705 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1992-259289/31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (USSH ) US DEPT HEALTH & HUMAN SERVICE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               08-OCT-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    08-OCT-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Polar; hydrophobic;
  22-DEC-1994
                                                                                                                                                                                                                                          cell epitope, P24M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3 KARVLAEAM 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 KARVLAEAM 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gag 357-370.
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9; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mukherjee
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                               (first entry)
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                                                                                                                                                         HIV-1; core protein; p24E; B-cell; vaccine; multimeric peptide; AIDS;
                                                                                                                                                                                                                                                                                                                                                                                                      peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 hydrolisation; inhibitor; therapeutic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AΒ
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Pred. No.
                                                                                                          type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
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0.19;
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                                                                                                                                                            antigen;
3D organisation
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RESULT 14
AAW25875
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This sequence represents the T-cell epitope, P24M, which may be linked to a B-cell epitope from the V3 (MN) loop from HIV-1. These chimeric peptides may then be used in the production of HIV-1 vaccines. These peptides sequences may also be used in the production of multimeric peptides in which the linear peptides are C-terminally modified by the addition of a Lys residue which is modified on its epsilon amino acid to carry an additional copy of the peptide molecule. The linear and multimeric peptides may be used for the treatment of AIDS by acting to displace the binding of HIV virus to human or animal cells or by disturbing the 3D organisation of the virus.
                                                                                  Chong
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel tandem synthetic HIV-1 peptide(s) - comprising T-cel epitope of gag protein linked to B-cell epitope of V3 loop protein of an HIV-I isolate
                                                             WPI;
                                                                                                                                                                                                                                                                                                        HIV T-helper
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Chong P,
Claim 1; Column 73; 41pp; English
                      Tandem synthetic HIV peptide(s) useful as immunogens - comprising gag protein T-cell epitope linked to env protein B-cell epitope
                                                                                                            (CONN-) CONNAUGHT LAB LTD.
                                                                                                                                    09-JUN-1994;
09-JUN-1993;
                                                                                                                                                                        09-JUN-1993;
                                                                                                                                                                                                17-JUN-1997
                                                                                                                                                                                                                       US5639854-A.
                                                                                                                                                                                                                                              Synthetic
                                                                                                                                                                                                                                                                     HIV; human immunodeficiency virus; gag; T-cell; B-cell; epitope; env; V3 loop; vaccine; determinant; chimaeric.
                                                                                                                                                                                                                                                                                                                                    22-OCT-1997
                                                                                                                                                                                                                                                                                                                                                            AAW25875
                                                                                                                                                                                                                                                                                                                                                                                  AAW25875 standard; peptide; 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         09-JUN-1993;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 KARVLAEAM 10
                                                             1997-332082/30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
9; Conserv
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                                                                                  Klein MH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                         determinant core peptide p24M.
                                                                                                                                                                                                                                                                                                                                 (first entry)
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                                                                                                                                   94US-0257528.
93US-0073378.
                                                                                                                                                                         9305-0073378.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         88.9%;
                                                                                     Sia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sia CDY
                                                                                     CDY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 40;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 16;
0.2;
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RESULT 15
AAW67391
ID AAW67391
XX AAW677
XX AAW677
XX AAW677
XX AAW677
XX AAW677
XX AAW67391
XX AAW67391
XX AAW67391
XX AAW67391
XX IDMNU
KW IDMNU
KW IDMNU
KW V3 1
XX V3 1
XX
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Best Local S
Matches 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  09-JUN-1994;
09-JUN-1993;
05-JUN-1995;
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      Sequence
                                                   The invention relates to a novel immunogenic composition for use in vaccines for the treatment of HIV-1 comprising an HIV-1-derived T-cell epitope linked to an HIV-1-derived B-cell epitope. The T-cell epitopes are generally designed based on the p24 core protein and the B-cell epitopes from the V3 loop of the gp120 protein from various HIV-1 strains. This peptide is a T-cell epitope derived from the HIV-1 strain MN p24 core protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1998-556461/47.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chong P,
                                                                                                                                                                                                                                                                                           Disclosure; Column 23-24; 40pp; English.
                                                                                                                                                                                                                                                                                                                                                                            Synthetic human immunodeficiency virus-1 peptide(s) - containing T-cell epitope and B-cell epitope(s) are candidate vaccines against
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US5817754-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HIV-1 peptide epitope p24M.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (CONN-) CONNAUGHT LAB LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        05-JUN-1995;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAW67391 standard; peptide; 15 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
mes 9; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     w
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KARVLAEAM 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Klein MH,
      15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
      ξ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               94US-0257528.
93US-0073378.
95US-0464329.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sia CDY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
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0.2;
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Query Match Best Local Similarity

88.9%;

Score 40; . DB 19; Pred. No. 0.2;

Length 15;

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Matches 9; Conservative 0; Mismatches 0;

QY 2 KARVLAEAM 10
| | | | | | | | |
Db 3 KARVLAEAM 11
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Indels

0;

Gaps

0

Search completed: March 13, 2003, 18:49:14 Job time : 26.5455 secs

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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                                                                                                                                                                                                                                                                                                                                   Result
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  444444444
                                                                                                                                        length: 2000000000
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1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*

2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*

3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*

4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*

5: /cgn2_6/ptodata/2/iaa/pcTUS_COMB.pep:*

6: /cgn2_6/ptodata/2/iaa/backfiles1.pep:*
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                                                                                                                                                                                                                                                                                                                        Length
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          US-08-467-881A-76
US-08-257-528B-47
US-08-460-602A-47
US-08-465-217A-47
US-08-465-217A-47
US-08-467-881A-77
US-08-467-881A-77
US-08-257-528B-77
US-08-257-528B-77
US-08-267-528B-77
US-08-460-602A-78
US-08-460-602A-78
US-08-460-602A-78
US-08-465-217A-78
US-08-465-217A-78
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0S-08-257-5288-76

0S-08-460-6028-76

0S-08-463-9668-76

0S-08-463-9178-76

0S-08-465-2178-76

0S-08-465-25078-76
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US-09-053-941-15
US-09-817-413-15
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-368	-625A	-625A-	867A	-459A	882-	-446-	625A)2142	.081-	981-	217-	625A-27	8812	881A	507A	507A	·329A	
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ALIGNMENTS

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; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-792-553-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 1
US-08-792-553-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 4, Application US/08792553 Patent No. 5981200 GENERAL INFORMATION:
 Query Match
Best Local Similarity
Matches 9; Conserv
                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIDM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Vei
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/792,553
FILING DATE: 31-JAN-1997
                                                                                                                                                                                             FILING DATE: 31-JAN-1997

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Lisa A. Haile, Ph.D.

REGISTRATION NUMBER: 38,347

REFERENCE/DOCKET NUMBER: 07257/041001/UC 96-160-2

TELECOMMUNICATION INFORMATION:

TELEPHONE: 619-678-5099

TELEPAX: 619-678-5099

INFORMATION FOR SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: Tandem time....
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: FISH & RICHARDSON P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Tsien, Roger Y.

APPLICANT: Heim, Roger

APPLICANT: Heim, Roger

APPLICANT: Heim, Roger
                                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: La Jolla
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  92037
       Conservative
88.9%; but
100.0%; Pr
                       Score 40; Pred. No.
         Mismatches
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                       DB 2;
0.033;
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                                       Length 10
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2 KARVLAEAM 10 |||||||| 1 KARVLAEAM 9

US-09-053-941-15

Application US/09053941

Sequence 15, Applica Patent No. 6271354 GENERAL INFORMATION:

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RESULT 4
US-09-147-208-21
; Sequence 21, Application US/09147208
                                                                                      밁
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                                                                                                                                                                                                             ORGANISM: Human immunodeficiency virus type 1
PUBLICATION INFORMATION:
JOURNAL: Meth. Enzymol.
VOLUME: 38
PACES: 299-
DATE: 1974
US-09-817-413-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Human immunodeficiency virus type 1
PUBLICATION INFORMATION:
JOURNAL: Meth. Enzymol.
VOLUME: 38
PAGES: 299
DATE: 1974
US-09-053-941-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          B
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                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: 60/043,380
PRIOR FILING DATE: 1999-04-03
NUMBER OF SEQ ID NOS: 25
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EARLIER FILING DATE: 1999-04-03
NUMBER OF SEQ ID NOS: 25
SOFTWARE: PATENTIN VET. 2.0
SEQ ID NO 15
LENGTH: 10
TYPE: PRT
                                                                                                                                                                   Query Match
Best Local 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 15, Application US/09817413 Patent No. 6436648
                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: SRINIVISAN, ALGARSAMY
APPLICANT: KOPROWSKI, HILARY
TITLE OF INVENTION: CHIMERIC VIRAL PROTEINS
FILE REFERENCE: Chimeric Viral Proteins
CURRENT APPLICATION NUMBER: US/09/053,941
CURRENT FILING DATE: 1998-04-02
EARLIER APPLICATION NUMBER: 60/043,380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: SRINIVISAN, ALGARSAMY
APPLICANT: KOPROWSKI, HILARY
TITLE OF INVENTION: CHIMERIC VIRAL PROTEINS
FILE REFERENCE: Chimeric Viral Proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/09/817,413
CURRENT FILING DATE: 2001-03-26
                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
                                                                                                                                                                                                                                                                                                                                               ENGTH: 10
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100.0%;
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Pred. No.
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                                                                                                                                                                 DB 4;
0.033;
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0.033;
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; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-147-208-21
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Best Local S
Matches 9
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GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 76,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: (416) 361-1398
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Rudolph, John R.
REGISTION NUMBER: 38,003
REFERENCE/DOCKET NUMBER: 78
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/09
FILING DATE: 02-MAR-1999
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:
ADDITION NUMBER: US/09/147, 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                   APPLICANT: SIA, Charles D.Y. APPLICANT: CHONG, Pele APPLICANT: KLEIN, Michel H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: Antiviral NUMBER OF SEQUENCES: 71
CORRESPONDENCE ADDRESS:
ADDRESSEE: BERESKIN 6 PARR
CLASSIFICATION:
ATTORNEY/AGENT INI
                                                                                                                                                                                                                        STREET: Suite CITY: Toronto
                                APPLICATION NUMBER: US/0 FILING DATE: 09-JUN-1994
                                                                                                                                                                                        COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
les 9; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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CITY: Toronto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: Canada
ZIP: M5H 3Y2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STATE: Ontario
                                                                                                                                                                                                                                                            ADDRESSEE:
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                                                                                                                                                                       MSG 1R7
                                                                                                                                                                                                        Ontario
                                                                                                                                                                                                                                                                                                                                                                                                                Application US/08257528B
                                                                                                                                                                                                                                   E: Sim & McBurney
Suite 701, 330 University Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     40 King Street West
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
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 INFORMATION:
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                                                 US/08/257,528B
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                                                                                     Version #1.25
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Query Match
Best Local Similarity
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                                   US-08-460-602A-76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 6
US-08-460-602A-76
                                                              TELEFAX: (416) 595-1163
INFORMATION FOR SEQ ID NO: 7
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
STRANDEDNESS: single
   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: 1038-336 MIS:jb TELECOMMUNICATION INFORMATION: TELEPHONE: (416) 595-1155
                                                                                                                                                                                                                    CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: STEWART, MICHAEL I.
                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: (
FILING DATE: 09-JUN-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: Tandem Synthetic HIV-1 Peptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
                                                                                                                                                                 REFERENCE/DOCKET NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 10
REFERENCE/DOCKET NUMBER: 110
REFERENCE/TOCKET NUMBER: 115
                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/0: FILING DATE: 02-JUN-1995 CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET: Suite 7
CITY: Toronto
STATE: Ontario
                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: 08/257,528 FILING DATE: 09-JUN-1994
                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: 424
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                                                                                                                                                           TELEPHONE:
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M5G 1R7
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KLEIN, Michel H.
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ilarity 100.0%;
Conservative
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ກາດ: 76:
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   Score 40;
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Length 15;
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Best Local Similarity
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                                          US-08-465-217A-76
                                                        RESULT 8
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US-08-463-966A-76
          Sequence 76 Patent No.
                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/073,378

PILING DATE: 09-JUN-1993

CLASSIFICATION: 424

ATTORNEY/AGERT INFORMATION:

NAME: STEWART, MICHAEL I.

REGISTRATION NUMBER: 24,973

REFERENCE/DOCKET NUMBER: 1038-487 MIS:jb

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                 TELEFAX: (416) 595-11 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
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SOFTWARE: Patentin Rel
CURRENT APPLICATION DATA:
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CORRESPONDENCE ADDRESS: Sim 6 McBurney
STREET: Suite 701, 330 Un
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APPLICATION NUMBER: 08/257,528
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APPLICANT: KLEIN, Michel H.
TITLE OF INVENTION: Tandem Synthetic HIV-1 Peptides
                                                                                                   2 KARVLAEAM 10
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3 KARVLAEAM 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 0 CLASSIFICATION:
                                                                                                                                                                                                                                                    STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER:
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276, 580082
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                          Application US/08465217A
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IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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GENERAL

INFORMATION:

APPLICANT: SIA, Charles APPLICANT: CHONG, Pele

SIA, Charles D.Y.

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; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-465-217A-76
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                                                                                                                                                                                                                                                                                                                       Sequence 76, Application US/08464329A Patent No. 5817754
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APPLICANT: SIA, C
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ATTORNEY/AGENT INFORMATION:
NAME: STEWART, MICHAEL I
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038
TELECOMMUNICATION INFORMATION:
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NFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                     tent No.
                                                                                                                                                      CORRESPONDENCE ADDRESS:
ADDRESSEE: Sim & McBurney
STREET: Suite 701, 330 University Avenue
                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS LENGTH: 15 amino acids
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOPTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/465,217A
                                                                                                                                                                                                               NUMBER OF SEQUENCES:
                                                                                                                                                                                                                            TITLE OF INVENTION: Tandem Synthetic HIV-1 Peptides
                                                                                                                                                                                                                                              APPLICANT: CHONG, Pele
APPLICANT: KLEIN, Michel H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/073,378
FILING DATE: 09-JUN-1993
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APPLICATION NUMBER: 08/257,528
FILING DATE: 09-JUN-1994
CLASSIFICATION: 424
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MEDIUM TYPE: Floppy dlsk
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TITLE OF INVENTION: Tandem
NUMBER OF SEQUENCES: 101
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
les 9; Conserv
                                                                                                                                     STREET: Suite
CITY: Toronto
                                                                                                                       STATE: Ontario
                COMPUTER: IBM PC compatible OPERATING SYSTEM: PC DOS/MS-DOS
                                                                                                      COUNTRY:
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ZIP: M5G 1R7
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CITY: Toronto
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PatentIn Release #1.0, Version #1.25
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100.0%; Pred. No.
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RESULT 10
US-08-462-507A-76
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US-08-464-329A-76
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                                                                  APPLICATION UNMER: 08/257,
FILING DATE: 09-JUN-1994
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/073
FILING DATE: 09-JUN-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
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                                                                                                                                                 CLASSIFICATION: 424
PRIOR APPLICATION DATA:
08/257,528
                                                                                                                                                                                                                                      SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSEE: Sim & McBurney
STREET: Suite 701, 330 University Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
STRANDEDNESS: single
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APPLICATION NUMBER: 08/257,528
FILING DATE: 09-JUN-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: Tandem Synthetic HIV-1 Peptides NUMBER OF SEQUENCES: 101
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REFERENCE/DOCKET NUMBER: 10
TELECOMMUNICATION INFORMATION:
                                         ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: CHONG, Pele
APPLICANT: KLEIN, Michel H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: 424
PRIOR APPLICATION DATA:
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                                                            CLASSIFICATION:
                                                                                                                                                                                                      APPLICATION NUMBER: US/08/462,507A FILING DATE: 05-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                      CITY: Toronto
STATE: Ontario
                                                                                                                                                                                                                                                                       OPERATING SYSTEM:
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                                                                                                                                                                                                                                                                      IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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MICHAEL 1.
24,973
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100.0%; Pr
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US-08-462-507A-76
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                                 Query Match
   Matches
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LENGTH: 15 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: (416) 595-11 INFORMATION FOR SEQ ID NO:
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                                                                                                                      TELEFAX: (416) 595-1163
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/257
FILING DATE: 09-JUN-1994
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/073
FILING DATE: 09-JUN-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                NAME: STEWART, MICHAEL I.
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 10
TELECOMMUNICATION INFORMATION:
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APPLICANT: KLEIN, Michel H.
                                                                                                                                                                                                                                                             CLASSIFICATION: 424
NTTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ITLE OF INVENTION:
   Local Similarity 100. hes 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/08/467,881A FILING DATE: 06-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: M5G 1R7
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STATE: Ontario
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les 9; Conserv
                                                                                         TYPE: amino aci
STRANDEDNESS: s
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                                                                              OPOLOGY:
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Suite 701, 330 Un
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88.9%; Score 40;
100.0%; Pred. No.
tive 0; Mismatch
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Pred. No.
   Mismatches
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Best Local Similarity
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US-08-257-528B-47
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                                                                                                                                                                              Patent No. 5759769
GENERAL INFORMATION:
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COMPUTER READABLE FORM:
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ATTORNEY/AGENT INFORMATION:
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                                                                                         CORRESPONDENCE ADDRESS
                                                                                                                                     APPLICANT: CHONG, Pele
APPLICANT: KLEIN, Michel H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION:
                                                                                                       NUMBER OF SEQUENCES:
                                                                                                                         TITLE OF INVENTION:
                                                                                                                                                                   APPLICANT: SIA, Charles D.Y.
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CITY: Toronto
STATE: Ontario
                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 32 amino acids TYPE: amino acid STRANDEDNESS: single
                                            CITY: Toronto
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                                                             STREET:
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                 COUNTRY:
                                                                          ADDRESSEE:
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               Ontario
Canada
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                                                           Suite 701, 330 Un:
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KLEIN, Michel H.
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                                                                                                                       Tandem Synthetic HIV-1 Peptides
                                                                                                         101
                                                           330 University Avenue
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MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0
CURRENT APPLICATION DATA:
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Suite 701, 330 University Avenue
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88.9%; Score 40;
100.0%; Pred. No.
tive 0; Mismatc
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Best Local Similarity
Matches 9; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: 08/257
FILING DATE: 09-JUN-1994
CLASSIFICATION : 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/073
FILING DATE: 09-JUN-1993
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: STEWART, MICHAEL, I
                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM CC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 32 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                     CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION UNMBER: 08/257,528
FILING DATE: 09-JUN-1994
                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
ADDRESSEE: Sim & McBurney
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PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: 08/257,528
                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: Tandém Synthetic HIV-1 Peptides NUMBER OF SEQUENCES: 101
                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038-450 MIS: jb
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 595-1155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                              APPLICATION NUMBER: US/08/463,966A FILING DATE: 05-JUN-1995
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SOFTWARE: Patentin Polocy
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APPLICATION NUMBER:
                                        CLASSIFICATION:
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REGISTRATION NUMBER: 24,
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KLEIN, Michel H.
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08/073,378
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Pred. No.
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US-08-465-217A-47
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Patent No. 5
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                                                                                                                                                                                          CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/257,528
FILING DATE: 09-JUN-1994
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION DATA:
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APPLICATION DATA:
APPLICATION: 424
PRIOR APPLICATION: 424
CLASSIFICATION: 424
CLASSIFICATION: 424
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APPLICANT: SIA, C
                                                                  INFORMATION FOR SEQ ID NO:
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                                                                                                              REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 10
TELECOMMUNICATION INFORMATION:
                                                  SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/465,217A
                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 595-1155
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CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: STEWART, MICHAEL I.
NAME: STEWART, MICHAEL I.
103
104
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NUMBER OF SEQUENCES:
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   TYPE: amino acid
STRANDEDNESS: si
                                                                                               TELEPHONE:
                                                                                                                                                                                                                                                                                                                                          FILING DATE: 05-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STATE: Ontario
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CLASSIFICATION:
                                 ENGTH:
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                            32 amino acids
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                                                                                 (416)
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KLEIN, Michel H.
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Listing first 45 summaries
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US-10-101-464A-787
US-09-925-299-988
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                   Sequence 1127, Ap
Sequence 787, App
Sequence 988, App
Sequence 998, App
Sequence 1932, Ap
Sequence 93, Appl
Sequence 93, Appl
Sequence 344, Appl
Sequence 3475, A
Sequence 18, Appl
Sequence 15, Appl
Sequence 1532, A
Sequence 1819, Ap
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2,	125,	Sequence 125, App	Sequence 7, Appli	Sequence 12876, A	Sequence 12539, A	Sequence 5617, Ap		Sequence 35465, A	Sequence 36003, A	Ψ	Sequence 4, Appli	Sequence 4, Appli	ω ~	Sequence 12, Appl	Sequence 12, Appl	Sequence 10903, A	Sequence 1335, Ap		Sequence 8, Appli	Sequence 54, Appl	Sequence 8, Appli	Sequence 54, Appl	Sequence 8, Appli	Sequence 54, Appl	Sequence 8, Appli

ALIGNMENTS

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RESULT 2

US-10-101-464A-787

¡ Sequence 787, Application US/10101464A

¡ Publication No. US20030046728A1

¡ GENERAL INFORMATION:

¡ APPLICANT: Strabala, Timothy

¡ APPLICANT: Higgins, Colleen M.

¡ APPLICANT: Higgins, Compositions Isolated from Plant Cells

¡ TITLE OF INVENTION: and Their Use in the Modification of Plant Cell Signaling
                                                                                                                                                                                                                                                                                                                                                                                   ; NAME/KEY: SITE
; LOCATION: (124)
; OTHER INFORMATION:
US-09-764-864-1127
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APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins,
FILE REFERENCE: PTZ23
FILE REFERENCE: PTZ23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Prior application data removed - consult PALM or file wrapper NUMBER OF SEQ ID NOS: 1792
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/09/764,864 CURRENT FILING DATE: 2001-01-17
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TYPE: PRT
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PRIOR FILING DATE: 2000-11-01
PRIOR APPLICATION NUMBER: 09/228,986
PRIOR FILING DATE: 1999-01-12
PRIOR APPLICATION NUMBER: 60/162,866
PRIOR FILING DATE: 1999-11-01
PRIOR APPLICATION NUMBER: PCT/US00/00724
PRIOR FILING DATE: 2000-01-11
PRIOR FILING DATE: 2000-01-11
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NUMBER OF SEQ ID NOS: 1556
SOFTWARE: PAtentin Ver. 2.0
SEQ ID NO 988
LENGTH: 909
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 787
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TITLE OF INVENTION: Nucleic Acids, Proteins
FILE REFERENCE: PA102
CURRENT APPLICATION NUMBER: US/09/925,299
CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05883
PRIOR FILING DATE: 2000-03-08
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Best Local :
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CURRENT APPLICATION NUMBER:
CURRENT FILING DATE: 2002-0
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LOCATION: (47)
OTHER INFORMATION:
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OTHER INFORMATION:
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NAME/KEY: SITE
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196 AEQQNLKSQN 205
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SOFTWARE: PATENTIN VEr. 2
SEQ ID NO 988
LENGTH: 909
TYPE: PRT
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US-09-925-299-988
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Matches 7
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OTHER INFORMATION: >
NAME/KEY: SITE LOCATION: (851)
OTHER INFORMATION: >
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NAME/KEY: SITE
LOCATION: (52)
OTHER INFORMATION: 1
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CURRENT APPLICATION NUMBER: US/09/925,299
CURRENT FILING DATE: 2001-08-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: PCT/US00/05883
PRIOR FILING DATE: 2000-03-08
PRIOR APPLICATION NUMBER: 60/124,270
PRIOR FILING DATE: 1999-03-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: Nucleic Acids, Proteins
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NAME/KEY: SITE
LOCATION: (32)
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NAME/KEY: SITE
LOCATION: (851)
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NAME/KEY: SITE
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APPLICANT: Marnerakis, Margarita
APPLICANT: Carter, Darrick
APPLICANT: Fanger, Gary R.
APPLICANT: VedVick, Thomas S.
APPLICANT: WedVick, Thomas S.
APPLICANT: Bangur, Chaitanya S.
APPLICANT: McNabb, Andria
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.478C17
CURRENT APPLICATION NUMBER: US/09/902,941
CURRENT FILING DATE: 2001-07-10
NUMBER OF SEQ ID NOS: 2002
SOFTMARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1934
LENGTH: 464
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Best Local Similarity
Thes 6; Conserve
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-902-941-1932
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US-09-902-941-1932
US-09-902-941-1934
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CURRENT FILING DATE: 2001-07-10
NUMBER OF SEQ ID NOS: 2002
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 1932
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1934, Application.US/09902941 Patent No. US20020172952A1
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APPLICANT: McNabb, Andria
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIACNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.478C17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Henderson, Robert A. APPLICANT: Wang, Tongtong
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             TYPE: PRT
ORGANISM: Homo spaiens
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Fanger, Gary R.
Vedvick, Thomas S.
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Johnson, Jeffrey C.
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Watanabe, Yoshihiro
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Conservative
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; SEQ ID NO 93
; LENGTH: 162
; TYPE: PRT
; ORGANISM: Homo s
US-09-738-973-93
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US-09-854-133-93
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Best Local
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Best Local (
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Query Match
Best Local Similarity
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                                                                                                                 CURRENT APPLICATION NUMBER: US/09/738,973
CURRENT FILING DATE: 2000-12-14
NUMBER OF SEQ ID NOS: 587
SOFTWARE: FastSEQ for Windows Version 3.4
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TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
TITLE OF INVENTION: THE THERAPY AND DIAGNOSIS OF
FILE REFERENCE: 210121.475C10
                                                                                                                                                                         APPLICANT: Kalos, Michael D.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
TITLE OF INVENTION: THE THERAPY AND DIAGNOSIS OF
FILE REFERENCE: 210121.475C9
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APPLICANT:
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Kalos, Michael D.
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Elliot, Mark
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Secrist, Heather
Indirias, Carol Yoseph
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Lodes, Michael J.
Fling, Steven P.
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56.5%;
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Score 35;
Pred. No.
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DB 10;
44;
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               Length 162;
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US-09-864-761-33475
Sequence 33475, Application US/09864761
Patent NO. US20020048763A1
GENERAL INFORMATION:
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-986-480-344
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                         PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
PRIOR PPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR APPLICATION NUMBER: PCT/US01/00665
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PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR APPLICATION NUMBER: US 20/632,366
PRIOR APPLICATION NUMBER: US 20/632,366
PRIOR FILING DATE: 2000-10-04
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SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 344
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY FILE REFERENCE: AGOM1Ca-X-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
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nes 7; Conserv
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Pred. No.
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US-09-916-790-18
US-09-916-790-18
; Sequence 18, Application US/09916790
; Patent No. US20020061573A1
: GENERAL INFORMATION:
- GENERAL INFORMATION:
- ROY
                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Meyers, Rachael
APPLICANT: Kapeller-Libermann, Rosana
APPLICANT: Silos-Santiago, Immaculada
TITLE OF INVENTION: 18431 AND 32374, NOVEL HU
TITLE OF INVENTION: KINASE FAMILY MEMBERS AN
FILE REFERENCE: 381552002700
CURRENT APPLICATION NUMBER: US/09/916,790
CURRENT ELLING DATE: 2001-07-27
                                                                                ; OTHER INFORMATION: Consensus amino acid sequence US-09-916-790-18
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OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.87

OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.1

OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.1

OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.4

OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.4

OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 0.94

OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 6.3

OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.74

OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 4.1

OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 4.1

OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 4.1

OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 4.1

OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 4.1

OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 4.1

OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 4.1

OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 4.1
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Matches
                                                                                                                                                                                        SOFTWARE: FastSEQ for Windows Version SEQ ID NO 18
LENGTH: 341
TYPE: PRT
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LENGTH: 268
Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: 60/221,543 PRIOR FILING DATE: 2000-07-28
                                                                                                                                                                                                                                                                                                            NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Annomax Sequence Listing Engine vers.
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PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00662
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 1001-01-30
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                                                                                                                                       ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Homo sapiens
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OR FILING DATE: 2001-01-30
OR FILING DATE: 2001-01-30
OR FILING DATE: 2001-01-30
OR APPLICATION NUMBER: US 60/234,687
OR FILING DATE: 2000-09-21
OR FILING DATE: 2000-09-21
OR FILING DATE: 2000-06-30
OR FILING DATE: 2000-06-30
OR APPLICATION NUMBER: US 09/608,408
OR FILING DATE: 2001-01-29
OR FILING DATE: 2001-01-29
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)S: 37
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  Score 35; DB 10;
Pred. No. 1e+02;
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Matches

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US-09-801-574-42

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FILE REFERENCE: ELITRA.011A
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191.078
PRIOR FILING DATE: 2000-03-21
PRIOR PPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/207,727
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CURRENT FILING DATE: 2001-03-07
PRIOR APPLICATION NUMBER: 60/187,518
PRIOR FILING DATE: 2000-03-07
PRIOR APPLICATION NUMBER: 60/261,557
PRIOR FILING DATE: 2001-01-12
NUMBER OF SEO ID NOS: 90
SOFTWARE: FastSEQ for Windows Version 4.0
                                                    PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR APPLICATION NUMBER: 60/269,308
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APPLICANT: Wang, Peljing Jeremy
APPLICANT: Page, David C.
TITLE OF INVENTION: Reproduction-Specific Genes
FILE REFERENCE: 0399.2007-002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 11532, Application US/09815242 Patent No. US20020061569A1
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                                                                                                                                                                                                                                                                                                                        APPLICANT: Xu, H. Howard
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes
TITLE OF INVENTION: Prokaryotes
TITLE REFERENCE: ELITRA.011A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     09-815-242-11532
                                        PRIOR FILING DATE: 2001-02-16
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nes 8; Conserv
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Trawick, John D.
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Zyskind, Judith W.
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Pred. No. 1.4e+02;
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                                CURRENT APPLICATION NUMBER: US/09/736,457; CURRENT FILING DATE: 2000-12-13; NUMBER OF SEQ ID NOS: 1864; SOFTWARE: FastSEQ for Windows Version 3.0; SEQ ID NO 1819; LENGTH: 831; TYPE: PRT; ORGANISM: Homo sapiens
US-09-736-457-1819
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US-09-919-497-59
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US-09-815-242-11532
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US-09-736-457-1819
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US-09-919-497-59
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Patent No. US20020106662A1
GENERAL INFORMATION:
APPLICANT: Mutter, George L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQ ID NO 11532
LENGTH: 529
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GENERAL INFORMATION
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Query Match
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APPLICANT:
APPLICANT:
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PRIOR FILING DATE: 2000-07-31
NUMBER OF SEQ ID NOS: 100
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CURRENT APPLICATION NUMBER: US/09/919,497
CURRENT FILING DATE: 2001-07-31
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APPLICANT:
APPLICANT:
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                                                                                                                                                                                                   APPLICANT: Wang, Aijun
TITLE OF INVENTION: COMPOSITIONS AND METHODS
TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.478C15
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59 AEEMRMKSQE 68
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ERREWSRLKAKD 549
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Carter, Darrick
Retter, Marc
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Lodes, Michael
Fanger, Gary
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Pred. No. 2.4e+02;
Score 34;
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Pred. No. 3.6e+02;
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DB
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Length 831;
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GENERAL

APPLICANT:

APPLICANT:

APPLICANT: APPLICANT: Matches Query Match SEQ ID NO 42

TYPE: PRT ENGTH: 458

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Hacches 17. Compervative 2; Mismatches 3; Indels 0; Gaps 0;
Oy 2 PARCORLEGOL 13
Db 21 | 1 | 1 | 1 | 1 | 1 |
Db 23 FARANAVOROUJ 36

Search completed; March 13, 2003, 18:54:49

Job time: 12.1091 secs
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Title:
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Maximum DB
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      Score
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re greater than or equal to the score of the result being printed,
is derived by analysis of the total score distribution.
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1: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*

2: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*

3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*

4: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*

5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*

6: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*

7: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*

9: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*

9: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*

10: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*

11: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*

12: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*

13: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*

14: /cgn2_6/ptodata/1/pubpaa/US00_PUBCOMB.pep:*
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Listing first 45 s
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US-09-952-060-33
US-09-968-355-26
US-09-968-355-27
US-09-968-355-17
US-09-968-355-17
US-09-968-355-17
US-09-968-355-17
US-09-968-355-17
US-09-986-156-59
US-09-886-156-60
US-09-886-150-59
US-09-886-150-60
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US-09-886-150-60
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US-10-003-035-18
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Compugen Ltd.
Sequence 4, Appli
Sequence 8, Appli
Sequence 3, Appli
Sequence 18, Appli
Sequence 5, Appli
Sequence 20, Appli
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Sequence 59, Appli
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APPLICANT: HEIM, ROGER
APPLICANT: CUBITY, Andrew
TITLE OF INVENTION: TANDEM FLUORESCENT PROTEIN CONSTRUCTS
FILE REFERENCE: REGEN1260-3
CURRENT APPLICATION NUMBER: US/10/057,505
CURRENT FILING DATE: 2002-01-25
PRIOR APPLICATION NUMBER: US 08/792,553
PRIOR FILING DATE: 1997-01-31
PRIOR FILING DATE: 1997-01-31
PRIOR APPLICATION NUMBER: US 09/396,003
PRIOR FILING DATE: 1999-09-13
NUMBER OF SEQ ID NOS: 31
SOFTWARE: Patentin version 3.1
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US-10-057-505-4
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Best Local S
Matches 9
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Patent No. US20020164674A1
CEMERAL INFORMATION:
                                                                                                                                                                                                                                          SEQ ID NO 4
LENGTH: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: THE REGENTS OF THE UNIVERSITY OF CALIFORNIA APPLICANT: AURORA BIOSCIENCES CORPORATION APPLICANT: TSIEN, ROGER
                                                                                                                                                                                    TYPE: PRT ORGANISM: Artificial sequence FEATURE:
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               2 KARVLAEAM 10
KARVLAEAM
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9 US-09-860-846-41
10 US-09-861-289-41
110 US-10-127-516-12
9 US-10-127-516-12
9 US-10-27-629-12
10 US-09-815-626-11
10 US-09-815-626-11
10 US-09-815-242-5586
10 US-09-815-242-12789
10 US-09-815-242-10628
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0; Mismatches
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US-09-893-737-130

US-09-827-822-5

US-09-827-822-4
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RESULT 2 US-09-735-487-8 ; Sequence 8, Application US/09735487 ; Patent No. US20020042679A1

GENERAL INFORMATION:

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APPLICANT: PAUWELS, Rud1
TITLE OF INVENTION: METHOD OF MANAGING THE TITLE OF INVENTION: HIV POSTITIVE BASED ON TITLE OF INVENTION: OF HUMAN HIV STRAINS FILE REFERENCE: 1377-125P
CURRENT APPLICATION NUMBER: US/09/735,487
CURRENT FILING DATE: 2000-12-14
PRIOR APPLICATION NUMBER: 09/117,217
PRIOR APPLICATION NUMBER: 09/117,217
PRIOR FILING DATE: 1998-07-24
NUMBER OF SEQ ID NOS: 15
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SEO ID NO 8
LENGTH: 163
TYPE: PRT
ORGANISM: HIV-HXB2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 4, Application US/09756551A Patent No. US20020051768A1 GENERAL INFORMATION:
APPLICANT: C. MOTTOW et al.
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Best Local :
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                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/389,459
FILING DATE: 15-FEB-195
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/087,009
FILING DATE: 01-JUL-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/756,551A
FILING DATE: 08-JAN-2001
                                    ATTORNEY/AGENT INFORMATION:
NAME: Lauro, Peter C.
REGISTRATION NUMBER: 32,360
                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/987,867
FILING DATE: 09-DEC-1997
                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/376,184
FILING DATE: 17-AUG-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 28 STATE STREET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: ENCAPSIDATED RECOMBINANT VIRAL
TITLE OF INVENTION: UNCLEIC ACID AND METHODS OF MAKING AND
TITLE OF INVENTION: USING SAME
REFERENCE/DOCKET NUMBER: UAI-004CPDV2CN ELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                     CLASSIFICATION:
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Query Match
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; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-756-551A-4
                                                  ; ORGANISM: Human immunodeficiency virus type 1
US-10-003-035-18
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US-10-003-035-18
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US-09-827-822-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-827-822-3
                                                                                     SOFTWARE: PatentIn version 3.1
SEQ ID NO 18
LENGTH: 492
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQ ID NOS: 10
SOFTMARE: FASESEQ for Windows Version 3.0
SEQ ID NO 3
LENGTH: 294
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                Sequence 18, Application US/10003035
Patent No. US20020155127A1
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Query Match
Best Local Similarity
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                                                                                                                                                    CURRENT APPLICATION NUMBER: US/10/003,035
CURRENT FILING DATE: 2001-11-01
PRIOR APPLICATION NUMBER: 09/585,599
PRIOR FILING DATE: 2000-06-02
PRIOR APPLICATION NUMBER: PCT/US01/18238
PRIOR FILING DATE: 2001-06-04
UNMBER OF SED ID NOS: 75
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                                                                                                                                                                                                                                                                           APPLICANT: Wang, Danher TITLE OF INVENTION: GENETIC VACCINE AGAINST HUMAN IMMUNODEFICIENCY VIRUS FILE REFERENCE: 22488-712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: PEPTIDES THAT BLOCK VIRAL INFECTIVITY TITLE OF INVENTION: AND METHODS OF USE THEREOF FILE REFERENCE: TRIPEP.003A CURRENT APPLICATION NUMBER: US/09/827,822 CURRENT FILING DATE: 2001-04-06 PRIOR APPLICATION NUMBER: US/09/370,368 PRIOR APPLICATION NUMBER: US/09/370,368 PRIOR FILING DATE: 1999-08-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 275 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                           236 KARVLAEAM 244
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Pred. No.
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Pred. No.
Score 40;
Pred. No.
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0.57;
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APPLICANT: Keith, Paula
APPLICANT: Dryga, Sergey
APPLICANT: Caley, Ian
APPLICANT: Maughan, Maureer
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                                                                                                                                           APPLICANT: Kaslow, David C.
APPLICANT: Shiver, John W.
APPLICANT: Toner, Timothy J.
APPLICANT: Casimiro, Danilo R.
TITLE OF INVENTION: ENHANCED FIRST GENERATION ADENOVIRUS
TITLE OF INVENTION: VACCINES EXPRESSING CODON OPTIMIZED HIV1-GAG, POL, NEF
                                                  FILE REFERENCE: 20747Y
CURRENT APPLICATION NUMBER: US/09/952,060
CURRENT FILING DATE: 2001-09-14
PRIOR APPLICATION NUMBER: PCT/US01/28861
PRIOR FILING DATE: 2001-09-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Swanstrom, Ronald TITLE OF INVENTION: ALPHAVIRUS VECTORS AND VIROSOMES WITH MODIFIED HIV GENES FOR USE TITLE OF INVENTION: VACCINES FILE REFERENCE: 01113.000103 CURRENT APPLICATION NUMBER: US/09/991,258 CURRENT APPLICATION NUMBER: US/09/991,258 COURRENT FILING DATE: 2001-11-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR FILING DATE: 20 NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: 09/902,537
PRIOR FILING DATE: 2001-07-09
PRIOR APPLICATION NUMBER: 60/216,995
                                                                                                                                                                                                                                                                                   APPLICANT:
                                                                                                                                                                                                                                                                                                  APPLICANT: Emini, Emilio A. APPLICANT: Youil, Rima APPLICANT: Bett, Andrew J.
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                 PRIOR APPLICATION NUMBER: 60/317,814 PRIOR FILING DATE: 2001-09-07
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TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OTHER INFORMATION: Description of Artificial Sequence; No. US20020141975Ale OTHER INFORMATION: synthetic construct
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nes 9; Conserv
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 APPLICATION NUMBER: 60/279,056
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                                                                                                                                                                                                                                                                                                  Bett, Andrew J.
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Pred. No.
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US-09-968-355-20
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US-09-968-355-26
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US-09-952-060-33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: 60/236,273
PRIOR FILING DATE: 2000-09-28
NUMBER OF SEQ ID NOS: 26
SOFTWARE: PATENTIN VERSION 3.1
SEQ ID NO 26
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PRIOR APPLICATION NUMBER: 60/233,180
PRIOR FILING DATE: 2000-09-15
NUMBER OF SEQ ID NOS: 38
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 33
                                                                                                                                                                                                                          GENERAL INFORMATION:
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SEQ ID NO 20
LENGTH: 515
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Best Local (
                                                                   CURRENT APPLICATION NUMBER: US/09/968,355
CURRENT FILING DATE: 2001-09-28
PRIOR APPLICATION NUMBER: 60/236,273
PRIOR FILING DATE: 2000-09-28
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APPLICANT: Hunter, Eric
TITLE OF INVENTION: Chimeric Retroviral Gag Genes and Screening Assays
FILE REFERENCE: UAB-100XC1
CURRENT APPLICATION NUMBER: US/09/968,355
CURRENT FILING DATE: 2001-09-28
COURRENT FILING DATE: 2001-09-28
                                                                                                                                               APPLICANT: Sakalian, Michael
APPLICANT: Hunter, Eric
TITLE OF INVENTION: Chimeric Retroviral Gag Genes and Screening Assays
FILE REFERENCE: UAB-100XC1
                                NUMBER OF SEQ ID NOS: 26
SOFTWARE: PatentIn version 3.1
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TYPE: PRT
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TYPE: PRT
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nilarity 100.0%;
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Pred. No.
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; FEATURE:
NAME/KEY: MISC_FEATURE
LOCATION: (1)..(531)
OTHER INFORMATION: Ch3 amino acid sequence
US-09-968-355-23
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Best Local Similarity
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Sequence 17, Application US/09968355; Patent No. US20020094523A1; GENERAL INFORMATION:
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LENGTH: 531
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                                                                                                          SOFTWARE: PatentIn version 3.1 SEQ ID NO 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                      APPLICANT: Sakalian, Michael
APPLICANT: Hunter, Eric
TITLE OF INVENTION: Chimeric Retroviral Gag Genes and Screening Assays
FILE REFERENCE: UAB-100XC1
CURRENT APPLICATION NUMBER: US/09/968,355
CURRENT FILING DATE: 2001-09-28
CURRENT FILING DATE: 2001-09-28
                                                                                                                                           PRIOR APPLICATION NUMBER: 60/236,273 PRIOR FILING DATE: 2000-09-28 NUMBER OF SEQ ID NOS: 26
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CURRENT FILING DATE: 2001-09-28
PRIOR APPLICATION NUMBER: 60/236,273
PRIOR FILING DATE: 2000-09-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Sakalian, Michael
APPLICANT: Hunter, Eric
TITLE OF INVENTION: Chimeric Retroviral Gag Genes and Screening Assays
FILE REFERENCE: UAB-100XC1
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SOFTWARE: PatentIn version 3.1
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ORGANISM: Artificial Sequence
NAME/KEY: MISC_FEATURE LOCATION: (1)..(583)
                                          FEATURE:
                                                       ORGANISM: Artificial Sequence
                                                                         TYPE: PRT
                                                                                          LENGTH: 583
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ORGANISM: Artificial Sequence
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359 KARVLAEAM 367
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: Sequence 59, Application U:
: Patent No. US20020155127A1
: GENERAL INFORMATION:
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            CURRENT APPLICATION NUMBER: US/09/952,060
CURRENT FILING DATE: 2001-09-14
PRIOR APPLICATION NUMBER: PCT/US01/28861
PRIOR FILING DATE: 2001-09-14
PRIOR APPLICATION NUMBER: 60/317,814
PRIOR FILING DATE: 2001-09-07
PRIOR APPLICATION NUMBER: 60/279,056
PRIOR APPLICATION NUMBER: 60/279,056
PRIOR APPLICATION NUMBER: 60/279,056
PRIOR APPLICATION NUMBER: 60/233,180
PRIOR FILING DATE: 2001-03-27
PRIOR APPLICATION NUMBER: 60/233,180
PRIOR FILING DATE: 2000-09-15
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SOFTWARE: Patentin version 3.1
SEQ ID NO 59
LENGTH: 599
TYPE: PRT
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Matches 9; Conserv
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                                                                                                                                                                                                             APPLICANT: Shiver, John W.
APPLICANT: Toner, Timothy J.
APPLICANT: Casinitor, Danilo R.
TITLE OF INVENTION: ENHANCED FIRST GENERATION ADENOVIRUS
TITLE OF INVENTION: VACCINES EXPRESSING CODON OPTIMIZED HIV1-GAG, POL,
TITLE OF INVENTION: WODIFICATIONS
FILE REFERENCE: 20747Y
                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Emini, Emilio A. APPLICANT: Youil, Rima APPLICANT: Bett, Andrew J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Wang, Danher TITLE OF INVENTION: GENETIC VACCINE AGAINST HUMAN IMMUNODEFICIENCY VIRUS FILE REFERENCE: 22488-712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: PCT/US01/18238 PRIOR FILING DATE: 2001-06-04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/10/003,035
CURRENT FILING DATE: 2001-11-01
PRIOR APPLICATION NUMBER: 09/585,599
PRIOR FILING DATE: 2000-06-02
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SEQ ID NOS:
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Chen, Ling
                                                                                                                                                                                                                                                                                                                                               Kaslow, David C.
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APPLICANT: Eberle, Josef
APPLICANT: Brunn, Albrecht V.
APPLICANT: Hanapp, Stefan
APPLICANT: Hauser, Hans-Peter
TITLE OF INVENTION: RETROVIRUS FROM HIV GROUP AND ITS USE
FILE REFERENCE: 05495.0001-04
CURRENT APPLICATION NUMBER: US/09/886,156
CURRENT APPLICATION NUMBER: US/09/109,916
PRIOR APPLICATION NUMBER: US/09/109,916
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: DE P 42 33 646.5
PRIOR APPLICATION NUMBER: DE P 42 35 718.7
PRIOR APPLICATION NUMBER: DE P 42 35 718.7
PRIOR APPLICATION NUMBER: DE P 42 35 718.7
PRIOR APPLICATION NUMBER: DE P 42 44 541.8
PRIOR FILING DATE: 1992-10-22
PRIOR APPLICATION NUMBER: DE P 42 44 541.8
PRIOR FILING DATE: 1992-12-30
PRIOR APPLICATION NUMBER: DE P 43 18 186.4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; PRIOR FILING DATE: 1993-06-01
; NUMBER OF SEQ ID NOS: 67
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 59
; LENGTH: 498
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus
US-09-886-156-59
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; OTHER INFORMATION: Codon optimized gag-IA pol fusion
US-09-952-060-35
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US-09-886-156-60
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GENERAL INFORMATION:
APPLICANT: Guertler, Lutz G.
APPLICANT: Eberle, Josef
APPLICANT: Eberle, Josef
APPLICANT: Knapp, Stefan
APPLICANT: Knapp, Stefan
APPLICANT: Hauser, Hans-Peter
TITLE OF INVENTION: RETROVIES FROM HIV GROUP AND ITS USE
FILE REFERENCE: 05495.0001-04
CURRENT APPLICATION NUMBER: US/09/886,156
CURRENT FILING DATE: 2001-06-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 59, Application US/09886156 Patent No. US20020155428A1 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 80.0
Best Local Similarity 77.8
Matches 7; Conservative
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                                                                                                                                                                                                                         Sequence 60, Application US/09886156 Patent No. US20020155428A1
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Search completed: March 13, Job time: 9.54545 secs

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; SEQ ID NO 60
; LENGTH: 498
; TYPE: PRT
; ORGANISM: Human 1
US-09-886-156-60
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PRIOR FILING DATE: 1992-10-06
PRIOR APPLICATION NUMBER: DE P 42 35 718.7
PRIOR EILING DATE: 1992-10-22
PRIOR APPLICATION NUMBER: DE P 42 44 541.8
PRIOR APPLICATION NUMBER: DE P 42 44 541.8
PRIOR FILING DATE: 1992-12-30
PRIOR APPLICATION NUMBER: DE P 43 18 186.4
PRIOR FILING DATE: 1993-06-01
NUMBER OF SEQ ID NOS: 67
SOFTWARE: Patentin Ver. 2.0
                                                                                                           Query Match
                                                                          Matches
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358 KAKILAEAM 366
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                                    2 KARVLAEAM 10
                                                                                                                                                                  immunodeficiency virus
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                Sequence 130, App
Sequence 4, Appli
Sequence 8, Appli
Sequence 3, Appli
Sequence 18, Appli
Sequence 18, Appli
Sequence 5, Appli
Sequence 20, Appli
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Sequence 21, Appli
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Sequence 24, Appli
Sequence 35, Appli
Sequence 41, Appli
Sequence 4209, Appli
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Sequence 9, Appli	36		10316	e 447,	Sequence 5378, Ap	187,	e 29	Sequence 2, Appli	Sequence 81, Appl	84,	80,	Sequence 8, Appli	Sequence 13, Appl	Sequence 83, Appl	Sequence 13826, A	•	Sequence 59, Appl	Sequence 60, Appl	•	Sequence 60, Appl	Sequence 59, Appl	Sequence 60, Appl	Sequence 59, Appl	4	Sequence 5, Appli

ALIGNMENTS

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; TYPE: PRT; ORGANISM: Homo sapiens US-09-893-737-130
                                                                                                                                                                ; Sequence 4, Application US/10057505
; Patent No. US20020164674A1
                                                                                                                                                                                                         RESULT 2
US-10-057-505-4
                                           GENERAL INFORMATION:
APPLICANT: THE REGENTS OF THE UNIVERSITY OF CALIFORNIA APPLICANT: AURORA BIOSCIENCES CORPORATION
APPLICANT: HEIM, Roger
APPLICANT: HEIM, ROger
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 130, Application US/09893737 Patent No. US20020110855A1 GENERAL INFORMATION:
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Best Local Similarity
Matches 8; Conserv
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SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 130
LENGTH: 219
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APPLICANT: Presnell, Scott R.
TITLE OF INVENTION: MAMMALIAN SECRETED PROTEINS
FILE REFERENCE: 00-41
CURRENT APPLICATION NUMBER: US/09/893,737
CURRENT FILING DATE: 2001-06-28
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PRIOR APPLICATION NUMBER: US 60/215,446
PRIOR FILING DATE: 2000-06-30
APPLICANT: CUBITT, Andrew TITLE OF INVENTION: TANDEM FLUORESCENT PROTEIN CONSTRUCTS FILE REFERENCE: REGEN1260-3
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52 EKSRLLAEAA 61
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Pred. No. 1.5;
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NUMBER OF SEQ ID NOS:
SOFTWARE: Patentin Ve.
SEQ ID NO 8
LENGTH: 163
TYPE: PRT
ORGANISM: HIV-HXB2
US-09-735-487-8
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US-09-756-551A-4
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APPLICANT: HERTOGS, KURL
APPLICANT: HERTOGS, KURL
APPLICANT: HERTOGS, KURL
TITLE OF INVENTION: METHOD OF MANAGING THE
TITLE OF INVENTION: HIV POSTITIVE BASED ON
TITLE OF INVENTION: OF HUMAN HIV STRAINS
FILE REFERENCE: 1377-125P
CURRENT APPLICATION NUMBER: US/09/735,487
CURRENT FILING DATE: 2000-12-14
PRIOR APPLICATION NUMBER: 09/117,217
PRIOR FILING DATE: 1998-07-24
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; OTHER INFORMATION: Linker molety
US-10-057-505-4
                                                                                                                                                                        Sequence 4, Application US/09756551A Patent No. US2002005176BA1
GENERAL INFORMATION:
APPLICANT: C. MOXITOW et al.
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PRIOR FILING DATE: 1999-09-13
NUMBER OF SEQ ID NOS: 31
SOFTWARE: Patentin version 3.1
SEQ ID NO 4
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                               TITLE OF INVENTION: ENCAPSIDATED |
TITLE OF INVENTION: UUCLEIC ACID |
TITLE OF INVENTION: USING SAME
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 28 STATE STREET
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CURRENT FILING DATE: 2002-01-25
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PRIOR FILING DATE: 1997-01-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 10
TYPE: PRT
ORGANISM: Artificial sequence
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nes 8; Conserv
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mes 8; Conserv
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PatentIn Ver. 2.0
MASSACHUSETTS
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                                                                                                                                                                      Morrow et al
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                METHOD OF MANAGING THE CHEMOTHERAPY OF PATIENTS WHO ARE HIV POSTITIVE BASED ON THE PHENOTYPIC DRUG SENSITIVITY
                                                                                                          ENCAPSIDATED RECOMBINANT VIRAL NUCLEIC ACID AND METHODS OF MAKING AND USING SAME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         79.5%; Score 35; 100.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                       79.5%; Score 35; DB 10; Length 163; 100.0%; Pred. No. 4.4;
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                                                                         US-09-827-822-3
                                                                                                                                                                                                                                                                                                                                                                                                     US-09-827-822-3
                                                                                                                                      TITLE OF INVENTION: PEDTIDES THAT BLOCK VIRAL INFECTIVITY TITLE OF INVENTION: AND METHODS OF USE THEREOF FILE REFERENCE: TRIPEP.003A CURRENT APPLICATION NUMBER: US/09/827.822 CURRENT FILING DATE: 2001-04-06 PRIOR APPLICATION NUMBER: US/09/370,368 PRIOR FILING DATE: 1999-08-09 NUMBER OF SEQ ID NOS: 10 SOFTWARE: FastSEQ for Windows Version 3.0 SEQ ID NO 3
                                                                                                                                                                                                                                                                                                                        Sequence 3, Application US/09827822
Patent No. US20020091086A1
GENERAL INFORMATION:
APPLICANT: Anders Vahlne
Query Match
Best Local Similarity
Matches 8; Conserv
                                                                                      LENGTH: 294
TYPE: PRT
ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Lauro, Peter C.
REGISTRATION NUMBER: 32,360
REFERENCE/DOCKET NUMBER: UAI-004CPDV2CN
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 275 amino acids
TYPE: amino acid
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APPLICATION NUMBER: 08/389,459
FILING DATE: 15-FEB-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/987,867
FILING DATE: 09-DEC-1997
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APPLICATION NUMBER: 08/376,184
FILING DATE: 17-AUG-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            230 KARVLAEA 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: 08/087,009 FILING DATE: 01-JUL-1993
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79.5%; Score 35; DB 10; ilarity 100.0%; Pred. No. 8.7; Conservative 0; Mismatches 0
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(617) 742-4214
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                                                                                       Immunodeficiency Virus Type 1
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08-JAN-2001
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100.0%; Pr
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Pred. No.
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                                 Length 294;
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; TYPE: PRT
; ORGANISM: Human immunodeficiency virus type
US-10-003-035-18
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                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Johnston, Robert
APPLICANT: Davis, Nancy
APPLICANT: Swanstrom, Ronald
TITLE OF INVENTION: ALPHAVIRUS V
TITLE OF INVENTION: VACCINES
FILE REFERENCE: 01113.000103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 18, Application US/10003035
Patent No. US20020155127A1
GENERAL INFORMATION:
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: Olmsted, Robert
APPLICANT: Keith, Paula
APPLICANT: Dryga, Sergey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 5, Application US/09991258 Patent No. US20020141975A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/09/991,258
CURRENT FILING DATE: 2001-11-16
PRIOR APPLICATION NUMBER: 09/902,537
PRIOR FILING DATE: 2001-07-09
PRIOR APPLICATION NUMBER: 60/216,995
PRIOR FILING DATE: 2000-07-07
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CURRENT FILING DATE: 2001-11-01
PRIOR APPLICATION NUMBER: 09/585,599
PRIOR FILING DATE: 2000-06-02
PRIOR APPLICATION NUMBER: PCT/US01/18238
PRIOR FILING DATE: 2001-06-04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Wang, Danher TITLE OF INVENTION: GENETIC VACCINE AGAINST HUMAN IMMUNODEFICIENCY VIRUS FILE REFERENCE: 22488-712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQ ID NOS: 75
                                                                                                                                     LENGTH: 492
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
                                                                                                    OTHER INFORMATION: Description of Artificial Sequence; OTHER INFORMATION: synthetic construct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     339 KARVLAEA 346
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Caley, Ian
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                Conservative
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                               79.5%;
              Score 35; DB; Pred. No. 16; O; Mismatches
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                            VECTORS AND VIROSOMES WITH MODIFIED HIV GENES FOR USE
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US-09-952-060-33
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: 60/317,814
PRIOR FILING DATE: 2001-09-07
PRIOR APPLICATION NUMBER: 60/279,056
PRIOR FILING DATE: 2001-03-27
PRIOR APPLICATION NUMBER: 60/233,180
PRIOR FILING DATE: 2000-09-15
NUMBER OF SEQ ID NOS: 38
SOFTWARE: FastSEQ for Windows Version 4.0
                                                         SOFTWARE: Pate
SEQ ID NO 26
LENGTH: 500
TYPE: PRT
                                                                                                                                                                                                                                                                                  Sequence 26, Application US/09968355
Patent No. US20020094523A1
GENERAL INFORMATION:
APPLICANT: Sakalian, Michael
APPLICANT: Hunter, Eric
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Publication No.
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APPLICANT: Casimiro, Danilo R.
TITLE OF INVENTION: ENHANCED FIRST GENERATION ADENOVIRUS
TITLE OF INVENTION: VACCINES EXPRESSING CODON OPTIMIZED HIV1-GAG, POL,
TITLE OF INVENTION: WODIFICATIONS
FILE REFERENCE: 20747Y
                                                                                                                                    APPLICANT: Hunter, Eric
TITLE OF INVENTION: Chimeric Retroviral Gag Genes and Screening Assays
FILE REFERENCE: UAB-100XC1
CURRENT APPLICATION NUMBER: US/09/968,355
CURRENT FILING DATE: 2001-09-28
PRIOR APPLICATION NUMBER: 60/236,273
PRIOR FILING DATE: 2000-09-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT FILING DATE: 2001-09-14
PRIOR APPLICATION NUMBER: PCT/US01/28861
PRIOR FILING DATE: 2001-09-14
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TYPE: PRT
ORGANISM: Artificial Sequence
                   ORGANISM: Human immunodeficiency virus FEATURE:
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NAME/KEY: MISC_FEATURE
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                                                                                                                          PatentIn
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Shiver, John W.
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vo. US20030044421A1
                                                                                                                          version 3.1
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100.0%; Pr
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16;
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; NAME/KEY: MISC_FEATURE
; LOCATION: (1)..(531)
; OTHER INFORMATION: Ch3 amino acid sequence
US-09-968-355-23
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PRIOR APPLICATION NUMBER: 60/236,273
PRIOR FILING DATE: 2000-09-28
NUMBER OF SEQ ID NOS: 26
SOFTWARE: Patentin version 3.1
SEQ ID NO 20
LENGTH: 515
TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; FEATURE:
NAME/KEY: MISC_FEATURE
LOCATION: (1)..(515)
THER INFORMATION: Ch3a amino acid sequence
US-09-968-355-20
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Best Local Similarity
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; OTHER INFORMATION: HIV (FS-) GAG amino acid sequence US-09-968-355-26
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                                                                                                                                       NUMBER OF SEQ ID NOS: 26
SOFTWARE: PatentIn version 3.1
SEQ ID NO 23
LENGTH: 531
TYPE: PRT
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Query Match
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Best Local :
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                                                                                                                                                                                                                         APPLICANT: Sakalian, Michael
APPLICANT: Hunter, Eric
TITLE OF INVENTION: Chimeric Retroviral Gag Genes and Screening Assays
FILE REFERENCE: UAB-100XC1
CURRENT APPLICATION NUMBER: US/09/968,355
CURRENT FILING DATE: 2001-09-28
PRIOR APPLICATION NUMBER: 60/236,273
PRIOR APPLICATION NUMBER: 60/236,273
PRIOR FILING DATE: 2000-09-28
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CURRENT APPLICATION NUMBER: US/09/968,355
CURRENT FILING DATE: 2001-09-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Hunter, Eric TITLE OF INVENTION: Chimeric Retroviral Gag Genes and Screening Assays
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                                                                                                                        ORGANISM: Artificial Sequence
                                                                                                       FEATURE:
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DB 10;
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359 KARVLAEA 366

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CURRENT APPLICATION NUMBER: US/09/968,355
CURRENT FILING DATE: 2001-09-28
PRIOR APPLICATION NUMBER: 60/236,273
PRIOR FILING DATE: 2000-09-28
PRIOR FILING DATE: 2000-09-28
NUMBER OF SEQ ID NOS: 26
SOFTWARE: Patentin version 3.1
SEO ID NO 17
LENGTH: 583
TYPE: PRT
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US-09-968-355-17
; Sequence 17, Ap
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; Sequence 59, Application US/10003035
; Patent No. US20020155127A1
; GENERAL INFORMATION:
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; LCCATION: (1)..(583)
; OTHER INFORMATION: Chimera 4 amino acid sequence
US-09-968-355-17
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NUMBER OF SEQ ID NOS: 75
SOFTWARE: Patentin version 3.1
SEQ ID NO 59
LENGTH: 599
TYPE: PRT
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Patent No. US20020094523A1
GENERAL INFORMATION:
                               Matches
                                            Query Match
Best Local
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TITLE OF INVENTION: GENETIC VACCINE AGAINST HUMAN IMMUNODEFICIENCY VIRUS
FILE REFERENCE: 22448-712
CURRENT APPLICATION NUMBER: US/10/003,035
CURRENT FILING DATE: 2001-11-01
PRIOR APPLICATION NUMBER: 09/585,599
PRIOR APPLICATION NUMBER: PCT/US01/18238
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APPLICANT: Hunter, Eric
TITLE OF INVENTION: Chimeric Retroviral Gag Genes and Screening Assays
FILE REFERENCE: UAB-100XC1
                                                                                                           FEATURE:
OTHER INFORMATION: Gag-PI
                                                                                                                                      ORGANISM: Artificial sequence
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                       79.5%; Sc. 100.0%; Pr
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                                            Score 35;
Pred. No.
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Pred. No. 19;
0; Mismatches
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                               Mismatches
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; APPLICANT: Zhao, L.
; TITLE OF INVENTION: DNA encoding methymycin and pikromycin
; FILE REFERENCE: 600.438US1
; CURRENT APPLICATION NUMBER: US/09/860,846
; CURRENT FILING DATE: 2001-05-18
; PRIOR APPLICATION NUMBER: 09/105,537
; PRIOR FILING DATE: 1998-06-26
; NUMBER OF SEO ID NOS: 43
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 41
; LENGTH: 928
; TYPE: PRT
; ORGANISM: Streptomyces venezuelae
US-09-860-846-41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: KASIOW, David C.

APPLICANT: Shive, John W.

APPLICANT: Toner, Timothy J.

APPLICANT: Toner, Timothy J.

APPLICANT: Toner, Timothy J.

APPLICANT: Casimiro, Danilo R.

TITLE OF INVENTION: ENHANCED FIRST GENERATION ADENOVIRUS

TITLE OF INVENTION: VACCINES EXPRESSING CODON OPTIMIZED HIV1-GAG, POL, NEF AND

TITLE OF INVENTION: WODIFICATIONS

FILE REFERENCE: 20747Y

CURRENT FILING DATE: 2001-09-14

PRIOR APPLICATION NUMBER: PCT/US01/28861

PRIOR APPLICATION NUMBER: 60/217,814

PRIOR APPLICATION NUMBER: 60/217,814

PRIOR APPLICATION NUMBER: 60/279,056

PRIOR APPLICATION NUMBER: 60/279,056

PRIOR PILING DATE: 2001-03-27

PRIOR PILING DATE: 2001-03-27

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PRIOR PILING DATE: 2001-03-27
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US-09-952-060-35
; Sequence 35, Application US/09952060
; Publication No. US20030044421A1
; GENERAL INFORMATION:
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US-09-860-846-41
                                                                                                                                                                                                                                                                                                                                                                              Sequence 41, Application US/09860846
Patent No. US20020164/42A1
GENERAL INFORMATION:
APPLICANT: Sherman, D.H.
APPLICANT: Liu, H.
APPLICANT: Xue, Y.
APPLICANT: Xue, Y.
APPLICANT: Zhao, L.
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Best Local Similarity
Matches 8; Conserv
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PRIOR FILING DATE: 2000-09-15
NUMBER OF SEQ ID NOS: 38
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 35
                        Query Match
Best Local Similarity
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  75.0%;
77.8%;
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  Score 33;
Pred. No.
  DB 9;
84;
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                        Length 928;
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Search completed: March 13, 2003, 18:54:47 Job time: 9.54545 secs

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Sequence:
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876
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                                                          Q96LM3
Q9H0J4
Q99PHB
Q9WV90
Q9WV90
Q9LJE3
Q9RLJ63
Q9RL36
Q9L2F9
Q8C5V4
  Q9W5J8
                              Q940A5
Q97338
                                                  Q9V3Q9
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                                                                                                                                                                                                                                                                                                                                                                                                                                          summaries
                                                                                                                                                                                                SUMMARIES
Q961m3 homo sapien
Q9h0j4 homo sapien
Q9h0j4 homo sapien
Q9h0j4 homo sapien
Q9uph8 mus musculu
Q8xuul ralstonia s
Q9wv90 marmota mon
Q9lje3 arabidopsis
Q9rl16 streptomyce
Q8135 piromyces s
Q9l12f9 streptomyce
Q8554 oryza sativ
Q9v3g9 drosophila
Q940a5 arabidopsis
Q9138 physarum po
Q9hu50 pseudomonas
Q9vnm2 drosophila
Q9w5j8 drosophila
                                                                                                                                                                 Description
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Q9rv73 deinococcus	16 Q9RV73	267	66.0	33	5
Q8zuh2 pyrobaculum		216	٠	33	44
Q04365 mus musculu	11 004365	188	٠	33	3
Q8u3al pyrococcus	17 Q8U3A1	141	66.0	33	2
Q60729 mus musculu		96	•	33	41
Q902k1 human immun		84	•	33	0
Q9acb0 brucella ab	2 Q9ACB0	79-	٠	33	39
		\\ 25\	66.0	33	38.
060991 plasmodium 🔿	_	2228	68.0	34	37
ס		2148	68.0	34	36
~	13 Q90662	1604	68.0	34	35
Q8w056 oryza sativ	10 Q8W056	834	68.0	34	34
Q97wx9 sulfolobus		568	68.0	34	33
Q98ep9 rhizobium l		508	68.0	34	32
Q94il2 oryza sativ		394	68.0	34	31
	3 Q8TFW7	377	68.0	34	30
5	4 Q96PW6	370	68.0	<u>د</u>	29
082595 arabidopsis		328	68.0	34	28
0	10 Q94I10	324	68.0	34	27
Q9tzb0 caenorhabdi	5 Q9TZBO	294	68.0	34	26
ω	16 Q8RDQ3	281		34	25
	17 058626	159	68.0	34	24
Q8w6t7 bacteriopha	o	94	•	34	23
	17 Q9HQU2	74	68.0	34	22
	5 Q9V9D3	1486	•	35	21
Q95re5 drosophila		1486	70.0	35	20
Q967y2 drosophila	o	1486	70.0	35	19
i arabidopsi	10 Q9LVY5	1140	70.0	35	8
O83666 treponema p	16 083666	625	70.0	35	17

ALIGNMENTS

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RESULT 1

Q96LM3

ID Q96L

AC Q96L

DT 01-D

DT 01-D

DT 01-D

DT 01-D

CS HOMC

OC Euka

OC Mamm

OX NCBJ

RN [1]

RN [1]

RN [1]

RN HOTE

RA HOTE

RA WATE

RA WAT
RESULT 2
Q9H0J4
ID Q9H0
AC Q9H0
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Best Local S
Matches
Q9H0J4;
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Q96LM3;
Q1-DEC-2001 (TrEMBLrel. 19, Created)
Q1-DEC-2001 (TrEMBLrel. 19, Last sequence update)
Q1-DEC-2001 (TrEMBLrel. 19, Last annotation update)
CDNA FLJ25373 fis, clone TST01951.
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
MCBI_TaxID-9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE .
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                                                                                                                                                                                                            KELAELRES
                                                                                                                                                                                                                                                                                                                                                 Similarity
9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      410 AA;
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larity 100.0%; Pred. No. 8.
Conservative 0; Mismatches
                                       PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         46072 MW;
                                       PRT;
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                                       1663 AA.
                                                                                                                                                                                                                                                                                                                                                                                 DB 4; Length 410; 8.9;
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RESULT

Q99PHB

AC Q99PHB

DT Q0

DT 
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Q8XUU1
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Best Local Similarity 80.0
Matches 8; Conservative
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Best Local
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O99PHB;
01-JUN-2001 (TrEMBLrel. 1
01-JUN-2001 (TrEMBLrel. 1
01-JUN-2001 (TrEMBLrel. 1
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01-MAR-2001 (TrEMBLrel. 1
01-DEC-2001 (TrEMBLrel. 1
Hypothetical 180.8 kDa pr
DKFZP434P0316.
    Q8XUU1;
Q8XUU1;
01-MAR-2002
01-MAR-2002
01-MAR-2002
                                                                                                                                                                                                                                                                                                                                                             Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases EMBL; AF288572; AAG60016.1; - SEQUENCE 131 AA; 14538 MW; 7FB9C3E7242EB424 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus (Mouse).
Eukaryota; Metazoa; C
Mammalla; Eutheria; F
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"Towards a Catalog of Human Genes and Proteins: Sequencing and Analysis of 500 Novel Complete Protein Coding Human cDNAs."; Genome Res. 11:422-435(2001).
EMBL; AL136774; CAB66708.1; ...
Hypothetical protein.
SEQUENCE 1663 AA; 180826 MW; 62E1441FEF5C4DEE CRC64;
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DKFZP434P031b,
Homo sapiens (Human).
Homo sapiens, Hotazoa; Chordata; Metazoa; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Zeytun A., Nagarkatti M., Nagarkatti P.S.; "Isolation and characterization of a new naturally occuring Fas ligand that is functional and expressed only in membrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. STRAIN-C57BL/6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FasL isoform.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=21154917; PubMed=11230166;
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    (TrEMBLrel.) (TrEMBLrel.)
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Rodentia;
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Last sequence Last anno
Created)
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Pred. No.
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Pred. No.
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                                                                                         PRT;
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Best Local S
Matches 8
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Best Local S
Matches 8
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MEDLINE-21681879; PubMed-11823852;

A Salanoubat M., Genin S., Artiguenave F., Gouzy J., Mangenot S.,

A Arlat M., Billault A., Brottier P., Camus J.C., Cattolico L.,

A Chandler M., Choisne N., Claudel-Renard C., Cunnac S., Demange N.,

A Gaspin C., Lavie M., Moisan A., Robert C., Saurin W., Schiex T.,

A Siguier P., Thebault P., Whalen M., Wincker P., Levy M.,

A Weissenbach J., Boucher C.A.:

"Genome sequence of the plant pathogen Ralstonia solanacearum.";

I Nature 415:497-502(2002).

R EMBL; AL646073; CAD16803.1; -.

W SEQUENCE 264 AA; 28781 MW; F68F861312DD3F61 CRC64;
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NON_TER
SEQUENCE
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O9WV90; O1-NOV-1999 (TrEMBLrel. 12, Created)
O1-NOV-1999 (TrEMBLrel. 12, Last sequence up
O1-MAR-2002 (TrEMBLrel. 20, Last annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-20010026; PubMed-10540161; Hodgson P.D., Grant M.D., Michalak T.I.; "Perforin and Fas/Fas ligand-mediated cychronic woodchuck viral hepatitis."; Clin. Exp. Immunol. 118:63-70(1999). EMBL; AF152368; AAD38387.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR003636; TNF_abc.
InterPro; IPR000478; TNF_family.
Pfam; PF00229; TNF; 1.
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Mammalia; Eutheria;
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RSC3094 OR RS00547.
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                                                                   KELAELRES
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   KELPELRES
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169
                                                                                                                                   Conservative
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Rodentia;
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88.9%;
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ia; beta subdivision; Ralstonia
                                                                                                                            Score 36; DB; Pred. No. 33; 0; Mismatches
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f68f861312DD3f61 CRC64;
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O91JE3

O91JE3;

O1-CT-2000 (TrEMBLrel. 15, Last sequence update)

O1-CT-2000 (TrEMBLrel. 19, Last annotation update)

O1-DEC-2001 (TrEMBLrel. 19, Last annotation update)

Genomic DNA, chromosome 3, Pl clone: MRP15.

Arabidopsis thaliana (Mouse-ear cress).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;

Spermatophyta; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q9RL36 PRELIMINARY; EQ9RL36; Q9RL36; Q1-MAY-2000 (TrEMBLrel. 13, Crool-MAY-2002 (TrEMBLrel. 13, Laston-Jun-2002 (TrEMBLrel. 21, Laston-Jun-2003 (TremBLrel. 21, Laston-Jun-2003 (TremBLrel. 21, Laston-Jun-200451) R SCE51A.29C.
MEDLINE-9700/351; PubMed-8843436; Redenbach M., Kieser H.M., Denapaite D., Kinashi H., Hopwood D.A.; "A set of ordered cosmids and a detailed the 8 Mb Streptomyces coelicolor A3(2) ch Mol. Microbiol. 21:77-96(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Murphy L., Harris D.; Submitted (SEP-1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Streptomyces coelicolor.
Bacteria; Firmicutes; Actinobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence features of the region TAC and BAC clones.", DNA Res. 7:217-221(2000).
EMBL; AP000603; BAB01755.1; -.
SEQUENCE 265 AA; 30326 MW;
                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                       Thomson N.R., Parkhill Submitted (SEP-1999) to
                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-A3(2);
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Submitted (OCT-1999)
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STRAIN=A3(2) / M145;

STRAIN=A3(2) / M145;

Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,

Bentley S.D., Chater K.D., Harris D.E., Quail M.A., Kleser H.,

Thomson N.R., James K.D., Harris D.E., Quail M.A., Kleser H.,

Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,

Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,

Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neil S.,

Rabbinowitsch E., Rajandream M.A., Rutherford K., Rutter S.,

Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,

warren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.,
                                                                                                       NADD(+) = 2-ACETO-2-HYDROXYBUTYRATE + NADPH).
EMBL; Y16743; CAA76356.1; -.
HSSP; 001292; 10MG.
InterPro; IPR000506; AcH_isomrdctse.
Pfam; PF01450; I1VC; 1.
TIGRFAMS; TIGR00465; i1VC; 1.
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01-MAY-1999 (TrEMBLrel.
01-MAY-1999 (TrEMBLrel.
01-JUN-2002 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Complete genome sequence of the model actinomycete Streptomyces coelicolor A3(2).";
coelicolor A3(2).";
Nature 417:141-147(2002).

EMBL; AL121596; CAB56681.1; -.
EMBL; AL121596; CAB56681.1; -.
Interpro; IPRO01932; PP2C-11ke.
SMART; SM00332; PP2C-2; I.
SMART; SM00331; PP2C_SIG; 1.
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Eukaryota; Fungi; Ch
Neocallimasticaceae;
                                                                                  SEQUENCE
                                                                                                                                                                                                                                chytrid Piromyces sp.
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Hackstein J.H.P.;
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                                                                                                                                                                                                                                            'Cytosolic enzymes with a mitochondrial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       œ
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 1 KELAELRES 9
                                                                                                                                                                                     . Microbiol. 30:1017-1027(1998).

CATALYTIC ACTIVITY: 2,3-DIHYDROXYISOVALERATE + NADP(+) = 2-
ACETOLACTATE + NADPH (ALSO: 2,3-DHYDROXYACID-3-METHYLVALERATE
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Mismatches
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O1-OCT-2000 (TremBLrel. 15, Created)
O1-OCT-2000 (TremBLrel. 15, Last sequence up
O1-JUN-2002 (TremBLrel. 21, Last annotation
Hypothetical protein SC02524.
SC02524 OR SCC127.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.

STRAIN-A3(2) / M.145;

Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,

Bentley S.D., Chater K.D., Harris D.E., Quail M.A., Kleser H.,

Thomson N.R., James K.D., Harris D.E., Quail M.A., Kleser H.,

Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,

Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,

Huang C.-H., Kleser T., Larke L., Murphy L., Oliver K., O'Neil S.,

Rabbinowitsch E., Rajandream M.A., Rutherford K., Rutter S.,

Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,

Warren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.,
                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
Wing R.A., Yu Y., Soderlund C., Chen M., Kim
Wasaki C., Henry D., Oates R., Simmons J.;
"Rice Genomic Sequence.";
"Rice Genomic Sequence.";
                                                                                                                                                                                                                                                                                                                                                                                                                  Oryza sativa (japonica cultivar-group).
Eukaryota; Viridiplantae; Streptophyta; En
Spermatophyta; Magnoliophyta; Liliopsida;
Ehrhartoideae; Oryzeae; Oryza.
NCBI_TaxID-39947;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q8S5V4 PRELIMINARY; PRT; 876 AA.
Q8S5V4;
Q8S5V4;
O1-JUN-2002 (TrEMBLrel. 21, Created)
O1-JUN-2002 (TrEMBLrel. 21, Last sequence update)
O1-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Hypothetical 97.8 kDa protein.
OJ1015F07.13.
                                                                                                                                                                                         Hypothetical protein. SEQUENCE 876 AA; 9
                                                                                                                                                                                                                                          Submitted (APR-2002) to the EMBL; AC104427; AAM19115.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Complete genome sequence of the model actinomycete Streptomyces coelicolor A3(2).";
Nature 417:141-147(2002).
EMBL; AL137166; CAB69745.1; -.
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Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
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253
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                                              KELAELRESTS
KELKELKEITS
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8; Conserv
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                                                                                                                                                                                              97835 MW;
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                                                                                                                    72.0%;
72.7%;
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Pred. No.
                                                                                                                 Score
Pred.
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                                                                                                                                                                                            26AE76D87C3E0180 CRC64;
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                                                                                               Mismatches
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                                                                                                                 No.
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                                                                                                                                                DB
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                                                                                                                                                                                                                                                                                                                                            H.-R.,
                                                                                                                                                                                                                                                                       databases
                                                                                                                                        Length 876;
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                                                                                            Indels
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RESULT OF THE CASE OF THE CASE
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RX Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Adams M.D., Celniker S.E., Holt R.W., Hoskins R.A., Galle R.F.,
RA Amanatides P.G., Scherer S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Bradon R.C., Rogers Y.H.C., Blazed R.G., Champe M., Pfeiffer B.D.,
RA Handen R.C., Rogers Y.H.C., Blazed R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Wan K.H., Basu A., Barman B.P., Bhandarl D., Bolshakov S.,
RA Ballew R.M., Basu A., Bather H., Coddeu E., Center A., Chandra I.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Barkva D., Botchan M.R., Bouck J., Brokstein P., Brottler P.,
RA Burtis K.C., Busam D.A., Butler H., Coddeu E., Center A., Chandra I.,
RA Cherry J.M., Castley S., Dahlke C., Davenport L.B., Davies P.,
RA Gerbill S., Deutschan M.R., Bouck J., Bayraktaroglu L., Besser K.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferritera S., Fleischmann W.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Hostin D., Houston K.A., Howland T.J., Hernandez J.R., Houck J.,
RA Hostin D., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Kimmel B.E., Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Mei M.H., Hoshrefi A.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Klamel B.E., Stenrik B., McIntosh T.C., McLeod M.P., McIsson D.L.,
RA Reinert K., Remington K.A., Sunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Stapleton M., Strong R., Sun E.,
RA Shue B.C., Stapleton M., Strong R., Wang X.,
Ra Park R., McC., Wang S., Park R.,
Ra Pa
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09V309;
01-MAY-2000
01-MAY-2000
01-JUN-2002
                                                                                                                                                        MEDLINE-99403001; PubMed-10471707;
Ashburner M., Misra S., Roote J., Lewis S.E., Blazej R., Davis T.,
Doyle C., Galle R., George R., Harris N., Hartzell G., Harvey D.,
Hong L., Houston K., Hoskins R., Johnson G., Martin C., Moshrefi A.,
Palazzolo M., Reese M.G., Spradling A., Tsang G., Wan K., Whitelaw K.,
Celniker S., Rubin G.M.;
"An exploration of the sequence of a 2.9-Mb region of the genome of
Drosophila melanogaster: the Adh region.";
Genetics 153:179-219(1999).
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Drosophila melanogaster (Fruit fly).
Eukaryota, Metazoa, Arthropoda, Tracheata, Hexapoda, Insecta,
Pterygota, Neoptera, Endopterygota, Diptera, Brachycera, Muscomorpha,
STRAIN-BERKELEY;
Celniker S.E., Agbayı
Butenhoff C., Champe
                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. STRAIN-BERKELEY;
                                                                                                SEQUENCE FROM
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   Agbayani /
Champe M.,
., Chavez
   Arcaina
lavez C.,
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   M., Ciesiolka L.,
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RA HOUSTON K.A., Hummasti S.R., Karra K., Kearney L., Kim E., Lee B.,
RA Lewis S., Li P., Lomotan M.A., Mazda P., Moshrefi A.R., Moshrefi M.,
RA Nixon K., Pacleb J.M., Park S., Pfeiffer B., Poon L., Sequeira A.,
RA Sethi H., Snir E., Svirskas R.R., Wan K.H., Weinburg T., Zhang R.,
RI Zieran L.L., Rubin G.M.;
RI Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
Submitted (MAR-2010).1; -.
DR EMBL; AE003461; AAF53431.1; -.
DR EMBL; AE003411; AAF44910.1; -.
DR EMBL; AE003411; AAF44910.1; -.
DR Fiyhase; FBgn0028924; GABA-B R1.
DR InterPro: IPR000337; GPCR_Mgr.
DR InterPro: IPR000037; GABA-B R1.
DR InterPro: IPR000037; GABA-B R1.
DR Pfam; PF00287; Na_K-ATPase_beta.
DR Pfam; PF00287; Na_K-ATPase; 1.
DR Pfam; PF00287; Na_K-ATPase; 1.
DR Pfam; PS0259; G_PROTEIN_RECEP_F3_4; 2.
                                                                                                                                                                                                                                                       Query Match
Best Local S
Matches 7
                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.

A Yamada K., Banh J., Banno F., Dale J.M., Goldsmith A.D., Lee J.M.,

A Yamada K., Banh J., Tang C., Toriumi M., Yamamura Y., Yu G.,

A Conodera C.S., Ouach H.L., Tang C., Toriumi M., Yamamura Y., Yu G.,

A Yu S., Bowser L., Carninci P., Chen H., Cheuk R., Hayashizaki Y.,

A Ishida J., Jones T., Kamiya A., Karlin-Neumann G., Kawai J., Kim C.,

A Koesema E., Lam B., Lin J., Meyers M.C., Miranda M., Narusaka M.,

A Nguyen M., Palm C.J., Sakurai T., Satou M., Seki M., Shinn P.,

A Nguyen M., Palm C.J., Sakurai T., Satou M., Seki M., Shinn P.,

A Southwick A., Tracy S.E., Shinozaki K., Davis R.W., Ecker J.R.,

A Southwick A., Tracy S.E., Shinozaki K., Davis R.W., Ecker J.R.,

A Southwick A., Tracy S.E., Shinozaki K., Davis R.W., Ecker J.R.,

A Southwick A., Tracy S.E., Shinozaki K., Davis R.W., Ecker J.R.,

B Southwick A., Tracy S.E., Shinozaki K., Davis R.W., Ecker J.R.,

A Southwick A., Tracy S.E., Shinozaki K., Davis R.W., Ecker J.R.,

B Southwick A., Tracy S.E., Shinozaki K., Davis R.W., Ecker J.R.,

B Southwick A., Tracy S.E., Shinozaki K., Davis R.W., Ecker J.R.,

B Southwick A., Tracy S.E., Shinozaki K., Davis R.W., Ecker J.R.,

B Southwick A., Tracy S.E., Shinozaki K., Davis R.W., Ecker J.R.,

B Southwick A., Tracy S.E., Shinozaki K., Davis R.W., Ecker J.R.,

B Southwick A., Tracy S.E., Shinozaki K., Davis R.W., Ecker J.R.,

B Southwick A., Tracy S.E., Shinozaki K., Davis R.W., Ecker J.R.,

B Southwick A., Tracy S.E., Shinozaki K., Davis R.W., Ecker J.R.,

B Southwick A., Tracy S.E., Shinozaki K., Davis R.W., Ecker J.R.,

B Southwick A., Tracy S.E., Shinozaki K., Davis R.W., Ecker J.R.,

B Southwick A., Tracy S.E., Shinozaki K., Davis R.W., Ecker J.R.,

B Southwick A., Tracy S.E., Shinozaki K., Davis R.W., Ecker J.R.,

B Southwick A., Tracy S.E., Shinozaki K., Davis R.W., Ecker J.R.,

B Southwick A., Tracy S.E., Shinozaki K., Davis R.W., Ecker J.R.,

B Southwick A., Tracy S.E., Shinozaki K., Davis R.W., Ecker J., Name R.,

B Southwick A., Tracy S.E., Shinozaki K., Davis R.W., Ecker J., N
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Best Local (
097338
097338;
01-MAY-1999
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation updat
Hypothetical 13.5 kDa protein.
AT1G06525.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Arabidopsis thaliana (Mouse-ear cress).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosid eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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                                                                                                                                                                                                                                                                                                                                                Hypothetical protein. SEQUENCE 120 AA; 13546 MW;
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les 8; Conserv
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(TrEMBLrel.
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                                                                                                                                                                                                                                                                          70.0%;
  10,
                                                                                                                                                                                                                                                     Score 35; DB Pred. No. 37; 1; Mismatches
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Pred. No. 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                DD4B45F932C66C33 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
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                                             317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        120
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                                                                                                                                                                                                                                                                                                  Length 120;
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20 STRAIN-ATCC 15692 / PAOL;

21 CARRAIN-20447337; PubMed-10984043;

22 REDLINE-20437337; PubMed-10984043;

23 Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrener P.,

24 A Stover R.L., Goltry L., Tolentino E. Westbrock-Wadman S., Yuan Y.,

25 A Garber R.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,

26 A Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,

27 Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,

28 A Reizer J., Saier M.H., Hancock R.E.W., Lory S., Olson M.V.;

27 "Complete genome sequence of Pseudomonas aeruginosa PAO1, an

28 Comportunistic pathogen.";

29 Tecorportunistic pathogen.";

20 Nature 406:959-964(2000).

20 REMBL; AR004926; AA608519.1; -.

20 Tecorportunistic pathogen.";

21 Tecorportunistic pathogen.";

22 Nature 406:959-964(2000).
Query Match
Best Local S
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q9HU50 PRELIMINARY;
Q9HU50;
Q1-MAR-2001 (TrEMBLrel. 16, C:
Q1-MAR-2001 (TrEMBLrel. 21, La
Q1-JUN-2002 (TrEMBLrel. 21, La
Probable carboxyl-terminal pro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bailey J., Cook L.J., Kilmer-Barber R., Swanston E., Solnica-Krezel L., Lohman K.N., Dove W.F., Dee J., Anderso "Identification of three genes expressed primarily during in Physarum polycephalum.", Arch. Microbiol. 172:364-376(1999).
EMBL; AJ133501; CAB39170.1; -.
                                                                                                       Protease;
SEQUENCE
                                                                                                                                                                                               InterPro; IPR001478; PD2.
InterPro; IPR004447; Protease_Cterm.
InterPro; IPR003581; TSPc.
Pfam; PF00595; PD2; 1.
SMART; SM00228; PD2; 1.
SMART; SM002245; TSPc; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-MAY-1999 (TrEMBLrel. 10, Last sequence update) 01-DEC-2001 (TrEMBLrel. 19, Last annotation update) Putative type II myosin heavy chain (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Putative type II myosin MYND.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pseudomonas aeruginosa.
Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Mycetozoa;
Physarum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Physarum polycephalum
                                                                                                                                                       TIGRFAMS; TIGR00225; prc; 1. PROSITE; PS50106; PDZ; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=287;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pseudomonas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PA5134.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=20059328; PubMed=10591846;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN-C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=5791;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          144 RELAELREKS 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14
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7; Conserv
  Similarity
7; Conserv
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                                                                                                       Complete 436 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  317 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                  proteome.
46018 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     36825 MW;
                       70.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     70.0%;
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Kilmer-Barber R.,
Dove W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Myxogastria; Myxogastromycetidae; Physarida;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (Slime mold).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gamma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           , Last sequence update) , Last annotation update) protease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2
                          Score 35;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 35; DB 5;
Pred. No. le+02;
2; Mismatches
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                                                                                                       D6347296673239B8 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             436
                       1.4e+02
                                                  DB 16;
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                                               Length 436;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Warrener P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               development
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Conservative

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Mismatches

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91

EDFAELQESTS 101

KELAELRESTS

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RESULT 15
ID VNM
AC 09VNM
AC 09VNM
DT 01-MJ
DT 0
В
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RA Addams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Addams M.D., Celniker S.E., Holt R.A., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Berndon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Ballew R.M., Basu A., Baxelala J., Bersktaroglu L., Belakin D.,
RA Ballew R.M., Basu A., Baxelala J., Bayaktaroglu L., Belakin D.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandarl D., Bolshakov S.,
RA Berkova D., Botchan M.R., Bouck J., Brokstein P., Botttier P.,
RA Berkova D., Botchan M.R., Buller H., Cadleu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L. B., Davles P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L. B., Davles P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L. B., Davles P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L. B., Davles P.,
RA Clodek A., Gong F., Gorrell J.H., Gu Z., Gunn P., Barris M.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Gunn P., Rarris M.,
RA Harris N.L., Harvey D., Hedman T.J., Hernandez J.R., Fleishmann W.,
RA Harris N.L., Harvey D., Hedman T.J., Hernandez J.R., Houck J.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Meinett K., Remington K.A., Haxon K., Nusskern D.R., Paleb J.M.,
RA Meinett K., Remington K.A., Haxon K., Nusskern D.R., Paleb J.M.,
RA Meinett K., Remington K.A., Nixon K., Nusskern D.R., Paleb J.M.,
RA Meng Z.-Y., Wassarman D.A., Welnistock G.M., Welson D.L.,
RA Wang Z.-Y., Wassarman D.A., Welnistock G.M., Welson D.L.,
RA Meng S.M., Wolf F., Sanger H., Zhong W., Zhong G., Zhao Q., Zheng L.,
RA Sheng X.H., Zhong W., Zhong X., Dan S., Zhu X., Smith H.O.,
RA Sheng S.H., Woodage T., Korly S., Zhu M., Sha S., Zhu X., Smith H.O.,
RA Sheng S., Sanger P., 
                                                                                                                                   Ouery Match
Best Local S
Matches 8
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
CG15589 protein.
CG15589.
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413
                                                                1 KELAELRESTS 11
KELNELRKPTS 423
                                                                                                                                       Similarity
8; Conserv
                                                                                                                                       Conservative
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                                                                                                                         Score 35; DB 5; Pred. No. 1.6e+02; 1; Mismatches 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
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                                                                                                                                                                                                    DB 5; Length 482;
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